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(54) Title: NOVEL STEROID-ACTIVATED NUCLEAR RECEPTORS AND USES THEREFOR

(57) Abstract

A novel nuclear receptor, termed the steroid and xenobiotic receptor (SXR), a broad-specificity sensing receptor that is a novel branch of the nuclear receptor superfamily, has been discovered. SXR forms a heterodimer with RXR that can bind to and induce transcription from response elements present in steroid-inducible cytochrome P450 genes in response to hundreds of natural and synthetic compounds with biological activity, including therapeutic steroids as well as dietary steroids and lipids. Instead of hundreds of receptors, one for each inducing compound, the invention SXR receptors monitor aggregate levels of inducers to trigger production of metabolizing enzymes in a coordinated metabolic pathway. Agonists and antagonists of SXR are administered to subjects to achieve a variety of therapeutic goals dependent upon modulating metabolism of one or more endogenous steroids or xenobiotics to establish homeostasis. An assay is provided for identifying steroid drugs that are likely to cause drug interaction if administered to a subject in therapeutic amounts.

5   NOVEL STEROID-ACTIVATED NUCLEAR RECEPTORS
                      AND USES THEREFOR

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FIELD OF THE INVENTION

The present invention relates to intracellular receptors, nucleic acids encoding
same, and uses therefor. In a particular aspect, the present invention relates to methods
for the modulation of physiological response to elevated levels of steroid and/or
15   xenobiotic compounds.

BACKGROUND OF THE INVENTION

Nuclear receptors constitute a large superfamily of ligand-dependent and
sequence-specific transcription factors. Members of this family influence transcription
either directly, through specific binding to the promoters of target genes (see Evans, in
20   Science 240:889-895 (1988)), or indirectly, via protein-protein interactions with other
transcription factors (see, for example, Jonat et al., in Cell 62:1189-1204 (1990),
Schuele et al., in Cell 62:1217-1226 (1990), and Yang-Yen et al., in Cell 62:1205-1215
(1990)). The nuclear receptor superfamily (also known in the art as the "steroid/thyroid
hormone receptor superfamily") includes receptors for a variety of hydrophobic ligands,
25   including cortisol, aldosterone, estrogen, progesterone, testosterone, vitamin D_3, thyroid

hormone and retinoic acid, as well as a number of receptor-like molecules, termed "orphan receptors" for which the ligands remain unknown (see Evans, 1988, supra). These receptors all share a common structure indicative of divergence from an ancestral archetype.

5   Lipophilic hormones such as steroids, retinoic acid, thyroid hormone, and vitamin D3 control broad aspects of animal growth, development, and adult organ physiology. The effects of these hormones are mediated by a large superfamily of intracellular receptors that function as ligand-dependent and sequence-specific transcription factors. The non-steroidal nuclear receptors for thyroid hormone (TR),

10   vitamin D3 (VDR), all-trans retinoic acid (RAR), and fatty acids and eicosanoids (PPAR) form heterodimers with the 9-cis retinoic acid receptor (RXR) that bind bipartite hormone-response elements (HREs) composed of directly repeated half sites related to the sequence AGGTCA (Mangelsdorf and Evans, *Cell* 83: 841-350, 1995). In contrast, the steroid receptors function as homodimers and bind to palindromic

15   target sequences spaced by three nucleotides (Beato et al., *Cell* 83: 851-857, 1995). In addition to the known receptors, a large group of structurally-related "orphan" nuclear receptors has been described which possess obvious DNA and ligand binding domains, but lack identified ligands (Mangelsdorf et al., *Cell* 83:835-839, 1995; Enmark and Gustafsson, *Mol. Endocrinol.* 10:1293 (1996); and O'Malley and Conneely,

20   *Mol. Endocrinol.* 6:1359 (1992)). Each has the potential to regulate a distinct endocrine signaling pathway.

           It is widely viewed that the hormone response is a consequence of the release, from an endocrine gland, of a ligand that circulates through the blood, and coordinately regulates responses in target tissues by acting through specific nuclear

25   receptors. Hormone responsiveness is dependent on the ability to rapidly clear ligand from the blood and the body so that, in absence of a stimulus, target tissues return to a ground state. Hormonal homeostasis is thus achieved by the coordinated release and degradation of bioactive hormones. Steroid hormones and their many metabolites are

primarily inactivated by reduction and oxidation in the liver. Since hundreds of adrenal steroids have been identified (e.g., dozens of each of the sex steroids (androgens, estrogens and progestins), 25-35 vitamin D metabolites, and likely hundreds of fatty acids, eicosanoids, hydroxyfats and related bioactive lipids), the problem of efficient ligand elimination is critical to physiologic homeostasis. In addition to the existence of a myriad of endogenous hormones, a similar diversity of ingested plant and animal steroids and bioactive xenobiotic compounds must also be degraded.

Selye first introduced the concept that exogenous steroids and pharmacologic substances may function to modulate the expression of enzymes that would protect against subsequent exposure to toxic xenobiotic substances (H. Selye, *J. Pharm. Sci.* 60:1-28, 1971). These compounds, which Selye called "catatoxic steroids," are typified by the synthetic glucocorticoid antagonist, pregnenolone-16-carbonitrile (PCN). PCN, and a variety of xenobiotic steroids, induce the proliferation of hepatic endoplasmic reticulum and the expression of cytochrome P450 genes (Burger et al., *Proc. Natl. Acad. Sci. (USA)* 89:2145-2149, 1992; Gonzalez et al., *Mol. Cell. Biol.* 6:2969-2976, 1986; and Schuetz and Guzelian, *J. Biol. Chem.* 259:2007-2012, 1984). One consequence of PCN treatment is the induction of nonspecific "protection" against subsequent exposure to such diverse xenobiotics as digitoxin, indomethacin, barbiturates, and steroids (Selye, *supra*, 1971).

Furthermore, it is known that a variety of such compounds can activate P450 genes responsible for their detoxification or degradation (Fernandez-Salguero and Gonzalez, *Pharmacogenetics* 5:S123-128, 1995; Denison and Whitlock, *J. Biol. Chem.* 270:18175-18178, 1995; O. Hankinson, *Ann. Rev. Pharmacol. Toxicol.* 35:307-340, 1995; and Rendic and Di Carlo, *Drug Metab. Rev.* 29:413-580, 1997).

While it appears that such catatoxic compounds regulate the expression of cytochrome P450s and other detoxifying enzymes, two lines of evidence argue that

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such regulation is independent of the classical steroid receptors. First, many of the most potent compounds (e.g., PCN, spironolactone, and cyproterone acetate) have been shown to be steroid receptor antagonists; whereas others (e.g., dexamethasone) are steroid receptor agonists (Burger, *supra*, 1992). Second, the nonspecific

5   protective response remains after bilateral adrenalectomy (and presumably in the absence of adrenal steroids), but not after partial hepatectomy (Selye, *supra*, 1971).

Insight into the mechanism by which PCN exerts its catatoxic effects is provided by the demonstration that PCN induces the expression of CYP3A1 and CYP3A2, two closely related members of the P450 family of monooxygenases (see, for example,

10 Elshourbagy and Guzelian in *J. Biol. Chem.* **255**:1279 (1980); Heuman et al., in *Mol. Pharmacol.* **21**:753 (1982); Hardwick et al., in *J. Biol. Chem.* **258**:10182 (1983); Scheutz and Guzelian in *J. Biol. Chem.* **259**:2007 (1984); Scheutz et al., in *J. Biol. Chem.* **259**:1999 (1984); and Gonzalez et al., in *J. Biol. Chem.* **260**:7435 (1985)). The CYP3A hemoproteins display broad substrate specificity, hydroxylating a variety of

15 xenobiotics (e.g., cyclosporin, warfarin and erythromycin), as well as endogenous steroids (e.g., cortisol, progesterone, testosterone and DHEA-sulfate. See, for example, Nebert and Gonzalez in *Ann. Rev. Biochem.* **56**:945 (1987) and Juchau in *Life Sci.* **47**:2385 (1990)). A PCN response element (which is highly conserved in the CYP3A2 gene promoter) has since been identified in subsequent studies with the cloned CYP3A1

20 gene promoter (see Miyata et al., in *Archives Biochem. Biophysics* **318**:71 (1995) and Quattrochi et al., in *J. Biol. Chem.* **270**:28917 (1995)). This response element comprises a direct repeat of two copies of the nuclear receptor half-site consensus sequence AGTTCA.

In addition to inducing CYP3A gene expression, PCN has also been shown to

25 have marked effects on hepatic cholesterol homeostasis. These effects include significant decreases in the levels of HMG-CoA reductase and cholesterol 7a-hydroxylase gene expression, with associated reductions in sterol biosynthesis and bile acid secretion. PCN has also been reported to enhance the formation of cholesterol

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esters and the hypersecretion of cholesterol into the bile. Thus, PCN affects key aspects of cholesterol metabolism, including its biosynthesis, storage and secretion.

Activation of orphan nuclear receptor(s) by catatoxic steroids provides a possible mechanism for the induction of xenobiotic metabolizing enzymes by compounds that do
5   not activate known steroid receptors. Because such enzymes are activated by high (pharmacological) doses of xenobiotic and natural steroids, such a "sensor" would be expected to be a broad-specificity, low-affinity receptor. Such receptors could be activated not only by endogenous steroids and metabolites but also by exogenous compounds such as phytosteroids, xenobiotics and pharmacologic inducers. Indeed, it is
10   known that a variety of such compounds can activate P450 genes responsible for their detoxification or degradation (see, for example, Fernandez-Salguero and Gonzalez in *Pharmacogenetics* 5:S123 (1995); Denison and Whitlock, Jr. in *J. Biol. Chem.* 270:18175 (1995); Hankinson in *Ann. Rev. Pharmacol. Toxicol.* 35:307 (1995); and Rendic and Di Carlo in *Drug Metab. Rev.* 29:413 (1997)).

15   In healthy individuals, steroid levels are tightly regulated, with increased catabolism of endogenous steroids being compensated by the pituitary releasing an increase of ACTH, which stimulates biosynthesis, and maintenance of plasma steroid levels. The increased catabolism is reflected by elevated urinary levels of steroid metabolites. Indeed, it is already known that treatment with rifampicin increases
20   urinary metabolites, such as 6β-hydroxycortisol (Ohnhaus et al., *Eur. J. Clin.* _ *Pharmacol.* 36:39-46, 1989; and Watkins et al., *J. Clin. Invest.*, 83:688-697, 1989), and bile acid metabolites, such as 6β-hydroxy hyocholic and 6α-hyodeoxycholic acids (Wietholtz et al., *J. Hepatol*, 24:713-718, 1996), while the plasma levels of many circulating steroids rise slightly due to increased synthesis (Lonning et al., *J. Steroid*
25   *Biochem.* 33:631-635, 1989; Bammel et al., *Eur. J. Clin. Pharmacol*, 42:641-644, 1992; and Edwards et al., *Lancet* 2:548-551, 1974).

When synthetic steroids, such as prednisolone (McAllister et al., *Br. Med. J.* 286:923-925, 1983; and Lee et al., *Eur. J. Clin. Pharmaco,.* 45:287-289,1993) or 17α-ethynylestradiol (F.P. Guengerich, *Life Sci.,* 47:1981-1988, 1990) are administered together with rifampicin, plasma levels are rapidly decreased due to enhanced urinary

5 clearance. In some patients undergoing rifampicin therapy for tuberculosis, the increase in urinary steroid levels has led to misdiagnosis of Cushing's syndrome (Kyriazopoulou and Vagenakis, *J. Clin. Endocrinol. Metab.,* 75:315-317, 1992; Zawawi et al., *Ir. J. Med. Sci.,* 165:300-302, 1996; and Terzolo et al., *Horm. Metab. Res.,* 27:148-150, 1995). In these patients, steroid production and clearance

10 normalized when rifampicin was withdrawn. In patients with Addison's disease, who mostly lack the ability to synthesize adrenal steroids, rifampicin treatment leads to rapid depletion of endogenous and administered steroids. These documented clinical situations confirm that induction of CYP3A4 causes increased steroid catabolism (Kyriazopoulou et al., *J. Clin. Endocrinol. Metab.* 59:1204-1206, 1984; and Edwards,

15 *supra,* 1974). However, the art is silent regarding the mechanism by which steroid metabolism is regulated in the body.

Although therapeutically administered steroids are beneficial in achieving therapeutic goals, such compounds can, in some cases, increase the overall level of steroids and xenobiotics above physiologically compatible levels in the subjects to

20 whom they are administered. In other cases, the increased level of steroids and/or xenobiotics may linger in the body longer than is therapeutically required. In addition, some subjects are treated with combinations of steroids and xenobiotics that may be administered separately to treat different conditions, but which, in combination, have an additive, or even synergistic, effect known as a drug interaction.

25 In such cases, the patient may be unaware when a physiologically incompatible level of steroids and xenobiotics has been reached, or when an otherwise therapeutic amount of a steroid becomes potentially dangerous due to combined effects of separately administered drugs.

Accordingly, there is still a need in the art for the identification and characterization of broad specificity, low affinity receptors that participate in the mediation of the physiological effect(s) of steroids and xenobiotics, particularly when combinations of such compounds disrupt homeostasis or cause drug interaction.

SUMMARY OF THE INVENTION

In accordance with the present invention, we have isolated and characterized an example of a novel class of human orphan nuclear receptor, termed the steroid and xenobiotic receptor (SXR). SXR is expressed almost exclusively in the liver, the primary site of xenobiotic and steroid catabolism. Unlike classical steroid receptors, SXR heterodimerizes with RXR and binds to directly repeated sequences related to the half-site, AGTTCA. SXR can activate transcription through response elements found in some steroid inducible P450 genes in response to an enormous variety of natural and synthetic steroid hormones, including antagonists such as PCN, as well as xenobiotic drugs, and bioactive dietary compounds, such as phytoestrogens. The ability of SXR to regulate expression of catabolic enzymes in response to this diversity of steroid and/or xenobiotic compounds provides a novel mechanism for direct regulation of metabolism so as to achieve physiologic homeostasis with respect to such steroid and/or xenobiotic compounds--ideal properties for a "steroid sensing receptor" which mediates the physiological effect(s) of hormones. SXR represents the first new class of steroid receptors described since the identification of the mineralocorticoid receptor ten years ago.

In accordance with a particular aspect of the present invention, there are also provided nucleic acid sequences encoding the above-identified receptors, as well as constructs and cells containing same, and probes derived therefrom. Furthermore, it has also been discovered that a wide variety of substrates modulate the transcription activating effects of invention receptors.

An important requirement for physiologic homeostasis is the removal and detoxification of various endogenous hormones and xenobiotic compounds with biological activity. Much of the detoxification is performed by cytochrome P450 enzymes, many of which have broad substrate specificity and are inducible by a

5   bewildering array of compounds, including steroids. The ingestion of dietary steroids and lipids induces the same enzymes and, thus, must be integrated into a coordinated metabolic pathway. Instead of possessing hundreds of receptors, one for each inducing compound, a class of broad-specificity, low-affinity nuclear receptors has been discovered that monitor total steroid levels and induce the expression of genes encoding

10   xenobiotic metabolizing enzymes. SXR, which is a member of a novel branch of the nuclear receptor superfamily, forms part of a steroid sensor mechanism for removal of elevated levels of steroids and/or xenobiotic compounds from circulation via broad-specificity, low-affinity receptors that represent a novel branch of the nuclear receptor superfamily.

15   **BRIEF DESCRIPTION OF THE FIGURES**

       Figure 1 illustrates that SXR is a novel orphan nuclear receptor.

       Figure 1A shows the sequence of the longest SXR cDNA clone (SEQ ID NO: 1) and a corresponding encoded protein (amino acids 41-434 of SEQ ID NO: 2). The DNA binding domain (amino acids 41-107) is shown in bold, and upstream

20   termination codons in frame with the putative initiator leucine are indicated by asterisks. That this Leu can function as an initiator was demonstrated by SDS-PAGE analysis of labeled proteins produced from *in vitro* transcribed, translated cDNAs. The unmodified cDNAs yielded a translation product indistinguishable in size from that produced when the leucine was changed to methionine, albeit not nearly as

25   efficient.

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Figure 1B presents a schematic comparison between SXR and other RXR partners (e.g., the *Xenopus* benzoate X receptor (xBXR), the human vitamin D3 receptor (hVDR), the human constitutively active receptor-alpha (hCARα), the rat farnesoid X receptor (rFXR), the human peroxisome proliferator activated receptor alpha (hPPARα),

5   the human liver-derived receptor X (LXR.α), the human retinoic acid receptor alpha-1 (hRARα-1), the human thyroid hormone receptor beta (hTRβ), the human retinoid X receptor alpha (RXRα) and the human glucocorticoid receptor alpha (hGRα)). Ligand-binding domain boundaries follow those for the canonical nuclear receptor ligand-binding domain (Wurtz et al., *Nature Struct. Biol.* 3:87-94, 1996). Similarity between

10   RXR and other receptors is expressed as percent amino acid identity (indicated in Arabic numerals above each clone). Amino acid residues in the sequences were aligned using the program GAP (Devereaux et al., *Nucl. Acids Res.* 12:387-395, 1984). DNA = DNA binding domain and LIGAND = ligand binding domain.

Figure 2 illustrates that SXR is activated by many steroids. Chimeric

15   receptors composed of the GAL4 DNA-binding domain and the SXR-ligand binding domain were cotransfected into CV-1 cells with the reporter gene tk(MH100)$_4$-luc (Forman et al., *Cell* 81:541-550, 1995). Results are shown as fold induction over solvent (DMSO) control for 50 μM of steroid and represent the averages and standard error from triplicate assays. Neither reporter alone, nor reporter plus GAL4-DBD,

20   was activated by any of these compounds. Column 1 = solvent; column 2 = corticosterone; column 3 = pregnenolone; column 4 = dihydrotestosterone (DHT); column 5 = dehydroepiandrosterone; column 6 = progesterone; column 7 = dexamethasone; column 7 = estradiol; column 8 = cortisol; and column 9 = cortisone.

Figure 3 illustrates the ability of steroidal activators to act additively. Thus, the

25   ability of steroidal activators to act additively was tested using full-length SXR and the reporter tk(LXRE)$_3$-luc (see Willy et al., in *Genes Dev.* 9:1033 (1995)). The cocktail contained 10 mM of each steroid for an overall concentration of 100 mM total steroid. The cocktail and its individual components were tested at 100, 10 and 1 mM; results are

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shown in the Figure for 100 mM cocktail and 10 mM aliquots of the component
steroids.

Figure 4 illustrates the broad activator and response element specificity of SXR.
Full-length SXR was tested in cotransfection experiments for its ability to activate
5   elements similar to those in Fig. 3 in response to a panel of steroids at 50 mM. DR-1,2
and TREp were only very slightly activated, hence results are shown only for
corticosterone and PCN. The data shown are expressed as mean fold induction over
solvent control +/- standard error from triplicate assays.

Figure 5 further illustrates the broad ligand specificity of SXR. Thus, it is seen
10   that reduction of the 4-5 double bond does not inactivate corticosterone. 6β-
hydroxylated, non-reduced, 5α and 5β reduced forms of corticosterone were tested for
their ability to activate GAL-SXR on tk(MH100)$_4$-luc and hGRa on MTV-luc at 50
mM. Similar results were obtained using full-length SXR.

Figure 6A-C are a series of illustrations indicating that SXR can activate
15   responsive elements found in various steroid and xenobiotic inducible P450 enzymes.

Figure 6A presents a schematic comparison of nucleotide sequences encoding
response elements found in inducible cytochrome P450 enzymes. A database search
for repeats of the sequence RGKTCA was performed and some of the matches for
enzymes involved in hepatic steroid hydroxylation are indicated. The standard
20   nomenclature for P450 enzymes has been utilized. P450R is the single P450
oxidoreductase required for hydroxylation of steroids. UGT1A6 is a rat uridine
diphosphate (UDP)-glucuronosyltransferase that conjugates glucuronic acid to
hydroxylated steroids.

Figure 6B presents a schematic comparison of conserved glucocorticoid-
25   response elements found in human CYP3 genes. The region of human CYP3A4
shown is necessary and sufficient for glucocorticoid and rifampicin induction of the

full-length promoter. Corresponding regions of CYP3A5 and CYP3A7 are shown (Barwick et al., *Mol. Pharmacol.* 50:10-16, 1996).

Figure 6C is a bar graph showing that SXR can activate through inducible, but not uninducible, CYP3 promoter elements. The ability of SXR to activate tk-

5   CYP3-luc response elements in response to various inducers was tested. Results are shown for 50 μM compound and represent the mean of triplicate determinations.

☐ = refampicin; and ■ = corticosterone

Figures 7A-C are bar graphs illustrating the ability of a panel of compounds to activate a representative of three members of the nuclear receptor superfamily,

10   human SXR (Figure 5A); mouse PXR (Figure 5B); and human estrogen receptor alpha (hERα). Results are shown for 50 μM of compound tested, except that the concentration of tamoxifen was 5 μM; and the concentration of dexamethasone (DEX) was 50 μM in Figures 7A and 7B and 5 μM in Figure 7C. Column 1 = solvent; column 2 = rifamipicin; column 3 = nifedipine; column 4 = tamoxifen;

15   column 5 = spironolactone; column 6 = PCN; column 7 = DEX;
column 8 = corticosterone; column 9 = cortisone; column 10 = DHT;
column 11 = estradiol; column 12 = DES; and column 13 = coumestrol.   ⎯

Figure 7D is a bar graph illustrating that reduction of the 4-5 double bond in corticosterone does not inactivate the compound as an agonist of hSXR. 6β-

20   hydroxylated, non-reduced, 5α and 5β reduced forms of corticosterone were tested for their ability to activate GAL- hSXR on tk(MH100)₄-luc (lefthand group of 5 columns) and hGRα on MTV-luc at 50 μM (righthand group of 5 columns). Similar results were obtained using full-length SXR. In each group of columns: column 1 = solvent; column 2 = corticosterone; column 3 = 5α-tetrahydrocorticosterone; column 4 = 5β-

25   tetrahydrocorticosterone; and column 5 = 6β-OH-corticosterone.

A DETAILED DESCRIPTION OF THE INVENTION

In accordance with the present invention, a new class of receptors has been identified that are part of the steroid/thyroid hormone superfamily of receptors, a representative member of which has been designated SXR (or "steroid X receptor").

5   Invention receptors are characterized by:

forming a heterodimer with retinoid X receptor (RXR),

binding to a (direct or inverted) repeat response element motif based on the half site AGTTCA,

activating transcription through response elements found in steroid inducible

10   P450 genes in response to a wide variety of natural and synthetic steroid hormones, and

being prominently expressed in the liver and the intestine.

Invention receptor(s) comprise a protein of approximately 464 amino acids (see SEQ ID NO:2), which is most closely, although distantly, related to the *Xenopus* benzoate X receptor (BXR), the vitamin D3 receptor (VDR) and the constitutively

15   activated receptor (CAR). Also provided herein is a 2068 bp cDNA which encodes an example of invention receptors (see SEQ ID NO:1 and Figure 1A).

In accordance with the present invention, there are also provided method(s) for modulating metabolism of one or more steroid and/or xenobiotic compound(s) in a subject in need thereof, comprising administering to the subject an effective amount

20   of a modulator of a SXR polypeptide that activates transcription of an endogenous gene operatively associated with a steroid and xenobiotic receptor X (SXR) response element.

In one particular aspect of the invention, a method is provided for preventing steroid toxicity in a subject undergoing treatment of a disease state involving therapeutic administration of one or more steroid compounds. In this embodiment, the invention method comprises administering to such a patient an effective amount of one or more agonists for an invention SXR polypeptide to activate transcription of an endogenous gene operatively associated with one of the invention SXR response elements, thereby preventing increase of the overall level of steroid and xenobiotics above a physiologically acceptable level. The steroid toxicity can result from dietary build-up. (e.g., of estrogens) from drug overdose, (e.g., caused by misdiagnosis of a disease state) or from a drug interaction between therapeutically administered compounds, or between one or more endogenous steroids and one or more dietary and/or therapeutically administered compounds.

Commonly administered therapeutic drugs that tend to accumulate or cause a drug interaction in certain individuals leading to an increase in the overall level of steroid and xenobiotics above a physiologically suitable level include tamoxifen, ralozifene (e.g., in treatment of breast cancer), vitamin K (e.g., in treatment of osteoporosis), and calcium channel blockers, such as nifedipine, and the like..

In yet another aspect, the invention provides a method for slowing clearance of a therapeutic steroid or xenobiotic from a subject, such as a human or other mammal, which comprises administering to the subject an effective amount of an antagonist for a SXR polypeptide that activates transcription of an endogenous gene operatively associated with a SXR response element. This aspect of the invention method is useful for controlling too rapid clearance of one or more therapeutic steroids and/or xenobiotics caused by a drug interaction between such compounds.

For example, rifampin (i.e., rifampicin), or an active derivative or analog thereof, is commonly used to treat tuberculosis. Yet rifampin tends to cause hepatic clearance of other therapeutic drugs, such as oral contraceptives (leading to unwanted

pregnancy), warfarin (leading to decreased prothrombin times), cyclosporine and prednisone (leading to organ rejection or exacerbations of any underlying inflammatory condition), and verapamil and diltiazem (necessitating increased dosage requirements). A similar situation develops in treatment of osteoporosis with the

5   therapeutic steroid Vitamin K. To overcome these problems, in accordance with the present invention, an effective amount of a SXR polypeptide antagonist is administered to the patient to slow clearance of the therapeutic steroids from the subject. '

In yet another aspect, the invention provides a screening assay for determining

10   whether a test compound, or a combination thereof, will activate the invention SXR polypeptide. The assay comprises contacting a host cell line containing an SXR receptor polypeptide, preferably a human or rabbit cell line, with one or more test compound(s) in an appropriate culture medium, wherein the host cell line further contains a reporter vector comprising a promoter that is operable in the cell line

15   operatively linked to an invention SXR response element for activation thereof, and DNA encoding a reporter protein operatively linked to the promoter for transcription of the DNA. The invention assay further includes determining whether the reporter protein is present (i.e., expressed by the cell line), wherein a determination that the reporter is present indicates the test compound activates the SXR polypeptide (i.e., an

20   agonist), and a determination that the reporter is not present in the assay predicts the test compound does not activate the invention SXR polypeptide (i.e. ,not an agonist).

It has been discovered that compound(s) that will activate transcription of the DNA contained in the above-described reporter vector are strong agonists of the invention SXR receptor and fall into the category of "steroids and/or xenobiotics" as

25   the term is used herein.

It has further been discovered that compounds determined by the above assay to activate transcription of the DNA contained in the above described reporter vector

are likely to become involved in a drug interaction if administered to a subject at a

therapeutic level. More particularly, there is a greater than 30% likelihood, for

example a likelihood of about 45% to about 90%, or from about 50% to about 70%,

that a therapeutic dose of such a compound will cause a drug interaction as described

5   herein, with other steroids and/or xenobiotics, whether such compounds are

endogenously produced, result from dietary sources, or are therapeutically

administered to a subject in treatment of a particular disease state. Therefore, in one

particular aspect, the invention assay is a method for screening compounds,

particularly potential therapeutic compounds, to determine those with at least a 30%

10   likelihood of becoming involved in an undesirable drug interaction if administered to

a subject at a therapeutic level. Such a screening assay is a valuable adjunct to any

drug development program because it will identify those drug candidates that must be

thoroughly screened *in vivo* to determine their safety, thereby reducing the cost of

drug development in general while preventing the possibility that a drug candidate

15   will prove potentially dangerous due to its capacity to cause unhealthy elevation of

steroid levels or too rapid clearance of another therapeutically administered compound

due to a "drug interaction."

       The invention methods are based upon the discovery of a new class of

receptors identified as part of the steroid/thyroid hormone superfamily of receptors.

20   The invention receptor, designated herein "the steroid and xenobiotic receptor"

(SXR), has been identified as a potential human homolog(s) of the Xenopus benzoate

'X' receptor, BXR (Blumberg et al., *Genes Dev.* 12:1269-1277, 1998). The cDNA

encoding one member of the SXR class (SEQ ID NO:1) predicts a protein of 434

amino acids (SEQ ID NO: 2) (Figure 1A), which is 73% identical to BXR in the

25   DNA-binding domain (DBD) and 43% identical in the ligand binding domain (LBD)

(Figure 1B). SXR is most closely related to the recently described pregnane 'X'

receptor (Kliewer et al., *Cell* 92:73-82, 1998) (95% identical in the DNA binding

domain (DBD), and 73% identical in the ligand binding domain (LBD). SXR is more

distantly related to the vitamin D3 receptor and the orphan receptor CAR (Baes et al.,

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Mol. Cell. Biol. 14:544-1551, 1994) (Figure 1B). Other than these receptors, SXR shows no more similarity to other nuclear receptors than the different receptor subfamilies do to each other (Figure 1B). It is known that true homologs among nuclear receptors typically share considerable similarity, especially in the DBD.

5   SXR can be further characterized as having a DNA binding domain of about 67 amino acids with 9 Cys residues (i.e., amino acid residues 41-107, as set forth in SEQ ID NO:2), wherein the SXR DNA binding domain has about 73 % amino acid identity with the DNA binding domain of the *Xenopus* benzoate X receptor. Alternatively, or in addition, SXR can be further characterized as having a ligand binding domain of at least

10   about 294 amino acids (i.e., at least amino acid residues 141-434, as set forth in SEQ ID NO:2), wherein said ligand binding domain has about 43 % amino acid identity with the ligand binding domain of the *Xenopus* benzoate X receptor (Figure 1B).

       A presently preferred SXR polypeptide according to the invention is a polypeptide having substantially the same amino acid sequence as shown in SEQ ID

15   NO:2. As employed herein, the phrase "substantially the same," whether used in reference to the nucleotide sequence of DNA, the ribonucleotide sequence of RNA, or the amino acid sequence of protein, refers to sequences that have slight and non-consequential sequence variations from the actual sequences disclosed herein. Species that are substantially the same are considered to be equivalent to the disclosed sequences

20   and as such are within the scope of the appended claims. In this regard, "slight and non-consequential sequence variations" means that sequences that are substantially the same as the DNA, RNA, or proteins disclosed and/or claimed herein are functionally equivalent to the sequences disclosed and/or claimed herein. Functionally equivalent sequences will function in substantially the same manner to produce substantially the

25   same compositions as the nucleic acid and amino acid compositions disclosed and claimed herein. In particular, functionally equivalent DNAs encode proteins that are the same as those disclosed herein or proteins that have conservative amino acid variations, such as substitution of a non-polar residue for another non-polar residue or a charged

residue for a similarly charged residue. These changes include those recognized by those of skill in the art not to substantially alter the tertiary structure of the protein.

An especially preferred SXR polypeptide according to the invention method is a polypeptide having the same amino acid sequence as shown in SEQ ID NO:2.

5   Thus, the terms "SXR receptor" and "SXR polypeptide" are interchangeable as used herein and are intended to include functional fragments of the invention SXR polypeptide(s). Such fragments include peptides having the DNA binding and/or the ligand binding properties of SXR, e.g., the DNA binding domain thereof (e.g., amino acid residues 71-107 as shown in SEQ ID NO:2), the ligand binding domain thereof
10   (e.g., amino acid residues 141-434 as shown in SEQ ID NO:2).

The modulator(s) useful in the practice of the invention method(s) include both agonists and antagonists of the SXR polypeptide. When the modulator is an agonist, the modulator is characterized as one which activates transcription of a gene encoding a compound active in catabolism of a therapeutic, endogenous, or dietary
15   steroid, or of certain dietary lipids, which gene is characterized by being associated with a SXR response element such that activation of the response element results in transcription of the gene. Generally the gene encodes an enzyme effective in metabolism of one or more steroids or xenobiotic substances, such as dietary lipids and phytoestrogens, and also includes a nucleotide sequence that encodes a SXR
20   response element, for example, one having a direct repeat of an AGGTCA half site (the DR half site) separated by a spacing of 3, 4, or 5 nucleotides, or a direct repeat of a one nucleotide variant thereof, such as a direct repeat of an AGTTCA half site (the βDR half site) separated by 3, 4, or 5 nucleotides. The response element can also comprise an inverse repeat of the half site AGGTCA separated by a 6 nucleotide
25   spacer, or an inverse repeat of a one nucleotide variant thereof, separated by a 6 nucleotide spacer. Examples of response elements suitable for use in practice of the invention methods can be selected from the following:

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DR-3,4,5 = AGGTCAN$_n$AGGTCA, wherein n is 3, 4, or 5 (SEQ ID NOS: 15, 16 and 17);

βDR-3,4,5 = AGTTCAN$_n$TGAACT, wherein n is 3, 4 or 5 (SEQ ID NO: 22); and

IR-6 = TGAACTN$_n$AGGTCA), wherein n is 6 (SEQ ID NO:23), and the like.

Those of skill in the art will recognize that any combination of nucleotides can be used to make up the 3, 4, 5, or 6 nucleotide spacer between the repeated half sites (i.e., N$_n$ in SEQ ID NOS: 15, 16, 17, 22 or 23).

Such response elements are generally found in genes encoding catabolic enzymes, such as CYP2A1, CYP2A2, CYP2C1, CYP3A1, CYP3A2, an P450 oxidoreductase, uridine diphosphate glucuronosyltransferase, or a glucuronosyl transferase, transcription of which genes is activated or suppressed by practice of the invention method(s).

Representative examples of agonists capable of activating transcription of such catabolic enzymes include molecules that have high-affinity receptors, such as progesterone, testosterone, estrogen and corticosterone, as well as their reduced catabolites that are, for the most part, inactive on the high-affinity receptors. In addition to the natural steroids, SXR is activated by synthetic steroids, including PCN and dexamethasone, as well as by xenobiotic drugs, phytosteroids, and the like. The presently preferred agonists include corticosterone, rifampicin, nifedipine, corticosterone, DES, estradiol, dihydrotestosterone, pregnenolone, progesterone, and PCN, with corticosterone being the strongest known activator.

When the modulator is an antagonist of SXR, the modulator functions in one or more of the following ways: (1) to block binding of the polypeptide to the SXR response element, (2) to inhibit formation of a heterodimer of the polypeptide and a retinoid X receptor, or (3) to inhibit binding of a ligand to the ligand binding domain

of SXR or an invention SXR polypeptide. For example, the antagonist can inhibit formation of a heterodimer between a retinoid X receptor and the SXR or an invention SXR polypeptide by blocking the docking site between the molecules. Alternatively, an antagonist can inhibits binding of a ligand to the ligand binding domain of the SXR or invention SXR polypeptide by binding to the active site of the ligand (i.e., the portion of the ligand that binds to the ligand binding domain). Any of a variety of compounds that will accomplish one or more of these goals can be used as an antagonist in the invention methods. For example, an antibody that binds to SXR or to a RXR so as to prevent formation of the a SXR:RXR heterodimer can be used as an antagonist in the practice of the present invention. Similarly, an antibody that blocks the ligand binding domain of the SXR receptor without activating transcription of the target gene so as to prevent binding of the ligand to the ligand binding domain will function as an antagonist in the invention method(s).

One of skill in the art will be aware of, or can readily devise, additional polypeptides or nucleotides that will act as antagonists of gene transcription in the invention method(s).

In accordance with another embodiment of the present invention, there are provided heterodimer complexes which consist of the above-described receptor polypeptide and RXR or other silent partner therefor.

In accordance with yet another embodiment of the present invention, there are provided isolated nucleic acids which encode the above-described receptor polypeptides. As used herein, the phrase "isolated nucleic acid" means a nucleic acid that is in a form that does not occur in nature. One means of isolating a nucleic acid encoding a polypeptide is to probe a mammalian genomic library with a natural or artificially designed DNA probe using methods well known in the art. DNA probes derived from the SXR gene are particularly useful for this purpose. DNA and cDNA molecules that encode SXR polypeptides can be used to obtain complementary genomic DNA, cDNA

or RNA from human, mammalian (e.g., mouse, rat, rabbit, pig, and the like), or other animal sources, or to isolate related cDNA or genomic clones by the screening of cDNA or genomic libraries, by methods described in more detail below. Examples of nucleic acids are RNA, cDNA, or isolated genomic DNA encoding SXR.

5   Exemplary DNAs include those which encode substantially the same amino acid sequence as shown in SEQ ID NO:2 (e.g., a contiguous nucleotide sequence which is substantially the same as nucleotides 583 - 1884 shown in SEQ ID NO:1). Presently preferred DNAs include those which encode the same amino acid sequence as shown in SEQ ID NO:2 (e.g., a contiguous nucleotide sequence which is the same as nucleotides 10   583 - 1884 shown in SEQ ID NO:1).

As used herein, nucleotide sequences which are substantially the same share at least about 90% identity, and amino acid sequences which are substantially the same typically share more than 95% amino acid identity. It is recognized, however, that proteins (and DNA or mRNA encoding such proteins) containing less than the above-15   described level of homology arising as splice variants or that are modified by conservative amino acid substitutions (or substitution of degenerate codons) are contemplated to be within the scope of the present invention. As readily recognized by those of skill in the art, various ways have been devised to align sequences for comparison, e.g., the Blosum 62 scoring matrix, as described by Henikoff and Henikoff 20   in *Proc. Natl. Acad. Sci. USA* **89**:10915 (1992). Algorithms conveniently employed for this purpose are widely available (see, for example, Needleman and Wunsch in *J. Mol. Biol.* **48**:443 (1970).

In accordance with still another embodiment of the present invention, there are provided nucleic acid constructs comprising the above-described nucleic acid, 25   operatively linked to regulatory element(s) operative for transcription of the nucleic acid and expression of the polypeptide in an animal cell in culture. There are also provided cells containing such a construct, optionally containing a reporter vector comprising:

21

(a)   a promoter that is operable in said cell,

(b)   a SXR response element, and

(c)   DNA encoding a reporter protein,

        wherein the reporter protein-encoding DNA is operatively linked to the

promoter for transcription of the DNA, and

        wherein the promoter is operatively linked to the SXR response element

for activation thereof.

        In accordance with a further embodiment of the present invention, there are

provided methods of making invention receptor polypeptide(s), said methods

comprising culturing cells containing an expression vector operable in said cells to

express a DNA sequence encoding said polypeptide.

        In accordance with a still further embodiment of the present invention, there are

provided probes comprising labeled single-stranded nucleic acid, comprising at least 20

contiguous bases in length having substantially the same sequence as any 20 or more

contiguous bases selected from bases 1 - 2068, inclusive, of the DNA illustrated in SEQ

ID NO:1, or the complement thereof. An especially preferred probe of the invention

comprises at least 20 contiguous bases in length having substantially the same sequence

as any 20 or more contiguous bases selected from bases 583 - 1884, inclusive, of the

DNA illustrated in SEQ ID NO:1, or the complement thereof.

        Those of skill in the art recognize that probes as described herein can be labeled

with a variety of labels, such as for example, radioactive labels, enzymatically active

labels, fluorescent labels, and the like. A presently preferred means to label such probes

is with ^{32}P. Such probes are useful, for example, for the identification of receptor

polypeptide(s) characterized by being responsive to the presence of one or more steroid

and/or xenobiotic to regulate the transcription of associated gene(s), said method

comprising hybridizing test DNA with a probe as described herein under high

stringency conditions (e.g., contacting probe and test DNA at 65°C in 0.5 M NaPO$_4$, pH

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7.3, 7% sodium dodecyl sulfate (SDS) and 5% dextran sulfate for 12-24 hours; washing
is then carried out at 60°C in 0.1xSSC, 0.1% SDS for three thirty minute periods,
utilizing fresh buffer at the beginning of each wash), and thereafter selecting those
sequences which hybridize to said probe.

5   In another aspect of the invention, the above-described probes can be used to
identify invention receptor polypeptide(s), or functional fragments thereof, said methods
comprising hybridizing test DNA with a probe as described herein under high
stringency conditions, and selecting those sequences which hybridize to said probe.

           In yet another aspect of the invention, the above-described probes can be used to
10   assess the tissue sensitivity of an individual to exposure to steroid and steroid-like
compounds by determining SXR mRNA levels in a given tissue sample. It is expected
that an individual having a high level of SXR mRNA (or protein) will be sensitive to the
presence of significant levels of steroid and xenobiotic compounds, such as are
encountered in many foods, or as a result of overproduction and/or reduced ability to
15   degrade steroids, as seen in such diseases as Cushing's syndrome, virilism and hirsutism
in females, polycystic ovarian syndrome, and the like.

           In accordance with yet another embodiment of the present invention, there are
provided antibodies which specifically bind the above-described receptor polypeptides.
Preferably, such antibodies will be monoclonal antibodies. Those of skill in the art can
20   readily prepare such antibodies having access to the sequence information provided
herein regarding invention receptors.

           Thus, the above-described antibodies can be prepared employing standard
techniques, as are well known to those of skill in the art, using the invention receptor
proteins or portions thereof as antigens for antibody production. Both anti-peptide and
25   anti-fusion protein antibodies can be used (see, for example, Bahouth et al. *Trends
Pharmacol Sci.* 12:338-343 (1991); Current Protocols in Molecular Biology (Ausubel et

al., eds.) John Wiley and Sons, New York (1989)). Factors to consider in selecting portions of the invention receptors for use as immunogen (as either a synthetic peptide or a recombinantly produced bacterial fusion protein) include antigenicity, uniqueness to the particular subtype, and the like.

5   The availability of such antibodies makes possible the application of the technique of immunohistochemistry to monitor the distribution and expression density of invention receptors. Such antibodies could also be employed for diagnostic and therapeutic applications.

          In accordance with a further embodiment of the present invention, binding
10   assays employing SXRs are provided, useful for rapidly screening a large number of compounds to determine which compounds (e.g., agonists and antagonists) are capable of binding to the receptors of the invention. Subsequently, more detailed assays can be carried out with initially identified compounds, to further determine whether such compounds act as agonists or antagonists of invention receptors.

15   The invention binding assays may also be employed to identify new SXR-like ligands. Test samples (e.g., biological fluids) may also be subjected to invention binding assays to detect the presence or absence of SXR or SXR ligands.

          Another application of the binding assay of the invention is the assay of test samples (e.g., biological fluids) for the presence or absence of SXR. Thus, for example,
20   tissue homogenates from a patient displaying symptoms thought to be related to over- or under-production of steroids can be assayed to determine if the observed symptoms are related to the presence of SXR.

          The binding assays contemplated by the present invention can be carried out in a variety of ways, as can readily be identified by one of skill in the art. For example,
25   competitive binding assays can be employed, as well as radioimmunoassays, ELISA, ERMA, and the like.

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In accordance with yet another embodiment of the present invention, there is provided a method of testing a compound for its ability to regulate transcription-activating effects of invention receptor polypeptide(s), said method comprising assaying for the presence or absence of reporter protein upon contacting of cells containing said

5   receptor polypeptide and reporter vector with said compound;

wherein said reporter vector comprises:

(a)   a promoter that is operable in said cell,

(b)   a hormone response element, and

(c)   DNA encoding a reporter protein,

10   wherein said reporter protein-encoding DNA is operatively linked to said promoter for transcription of said DNA, and

wherein said promoter is operatively linked to said hormone response element for activation thereof.

Hormone response elements suitable for use in the above-described assay

15   method comprise direct or inverted repeats of at least two half sites (each having the sequence RGBNNM, as defined herein). In each half site, RGBNNM:

R is selected from A or G;

B is selected from G, C, or T;

each N is independently selected from A, T, C, or G; and   —

20   M is selected from A or C;

with the proviso that at least 4 nucleotides of said -RGBNNM- sequence are identical with the nucleotides at corresponding positions of the sequence AGTTCA.

Those of skill in the art recognize that the spacing between half sites can vary

25   over a considerable range, typically falling in the range of about 0 up to 15 nucleotides. When the half sites are oriented as direct repeats, it is presently preferred that the half sites be separated by a spacer of 3, 4 or 5 nucleotides. Those of skill in the art recognize

that any combination of 3, 4 or 5 nucleotides can be used as the spacer. Direct repeat response elements having a spacer of 4 nucleotides (e.g., SEQ ID NOS:6, 7 or 16) are presently preferred. When the half sites are oriented as inverted repeats, it is presently preferred that the half sites be separated by a spacer of 4, 5 or 6 nucleotides. Those of
5   skill in the art recognize that any combination of 4, 5 or 6 nucleotides can be used as the spacer.

Optionally, the above-described method of testing can be carried out in the further presence of ligand for invention receptors, thereby allowing the identification of antagonists of invention receptors. Those of skill in the art can readily carry out
10   antagonist screens using methods well known in the art. Typically, antagonist screens are carried out using a constant amount of agonist, and increasing amounts of a putative antagonist (i.e., a competitive assay). Alternatively, antagonists can be identified by rendering the receptor constitutively active (e.g., by adding a strong, constitutively-active activator to the receptor) and screening for compounds which shut down the
15   resulting constitutively-active receptor.

In accordance with another aspect of the present invention, there are provided methods to identify compounds which are agonists of steroid X receptor (SXR), but which neither agonize nor antagonize other steroid receptors, said method comprising:

detecting in a first assay system the presence or absence of reporter-
20   protein upon contacting of cells containing SXR and reporter vector with said compound;

wherein said reporter vector comprises:

(a)   a promoter that is operable in said cell,

(b)   an SXR response element, and

25 .   (c)   DNA encoding a reporter protein,

wherein said reporter protein-encoding DNA is operatively linked to said promoter for transcription of said DNA, and

wherein said promoter is operatively linked to said SXR response element for activation thereof;

detecting in a second assay system the presence or absence of reporter protein upon contacting of cells containing a steroid hormone receptor other than SXR and reporter vector with said compound;

wherein said reporter vector comprises:

(a)   a promoter that is operable in said cell,

(b)   a response element for said receptor other than SXR, and

(c)   DNA encoding a reporter protein,

wherein said reporter protein-encoding DNA is operatively linked to said promoter for transcription of said DNA, and

wherein said promoter is operatively linked to said response element for said receptor other than SXR for activation thereof; and

identifying those compounds which induce production of reporter in said first assay, but not in said second assay, as compounds which are agonists of steroid X receptor (SXR), but neither agonists nor antagonists of other steroid receptors.

Thus, it can readily be seen that invention methods can be used to identify a variety of therapeutically useful compounds. The compounds identified as described herein can be used for the treatment of a wide variety of indications, such as, for example:

a)   Cushing's syndrome (hypercortisolism), which manifests as increased cortisol levels, leading to numerous problems including obesity, fatigue, hypertension, edema and osteoporosis;

b)   virilism and hirsutism in females due to overproduction of testosterone;

c)   androgen excess due to polycystic ovarian syndrome, which manifests as greatly increased circulating levels of dehydroepiandrosterone;

d)   enzymatic defects which lead to accumulation of specific steroids, such as:

1) 21-hydroxylase deficiency leading to increased synthesis of 17-hydroxy-progesterone and androgens;

2) 11β-hydroxylase deficiency leading to deoxycortisol and deoxycorticosterone accumulation and attendant hypertension;

3) 3β-hydroxysteroid dehydrogenase deficiency resulting in accumulation of pregnenolone and dehydroepi-androsterone, leading to sexual ambiguity in both sexes;

4) 17-hydroxylase deficiency, which prevents cortisol synthesis but leads to accumulation of corticosterone and deoxycorticosterone, resulting in hypertension and aberrant development of secondary sexual characteristics in both sexes;

f)   ameliorate the effect of substances in the diet and/or environment which act as endocrine disruptors, e.g., estrogens which may be involved in breast, colorectal and prostate cancers (Adlercreutz and Mazur in *Ann. Med.* 29:95-120 (1997); and the like.

Compounds which are specific agonists for SXR without acting as either agonists or antagonists for other steroid receptors will find particular utility where other steroid compounds have been used for their catatoxic properties, while tolerating the negative effects of such therapeutic use (presumably caused by the undesirable activation of previously described steroid receptors, e.g., glucocorticoid receptor).

Compounds which are specific agonists for SXR without acting as either agonists or antagonists for other steroid receptors will find particular utility where other steroid compounds have been used for their catatoxic properties, while tolerating the negative effects of such therapeutic use (presumably caused by the undesirable activation of previously described steroid receptors, e.g., glucocorticoid receptor).

In accordance with a still further embodiment of the present invention, there are provided methods for modulating process(es) mediated by invention receptor polypeptides, said methods comprising conducting said process(es) in the presence of at least one agonist, antagonist or antibody raised against invention receptor.

5   In accordance with yet another embodiment of the present invention, there are provided methods for inducing the expression of steroid degradative enzymes, said method comprising activating SXR. Exemplary steroid degradative enzymes contemplated for expression herein include steroid hydroxylases, and the like.

In accordance with the present invention, it has further been discovered that
10   induction of some xenobiotic-metabolizing enzymes by pharmacological levels of steroids is regulated by SXR, a class of broad-specificity, low-affinity, nuclear hormone receptors. One benefit of such a receptor-based system is that it induces the expression of xenobiotic metabolizing enzymes only at activator levels sufficiently high to interfere with normal endocrine function. It also makes biological sense that the expression of
15   enzymes with broad substrate specificity, such as cytochrome P450s, can be induced by a receptor responsive to a diverse group of activators, some of which can be substrates for the induced enzymes.

To determine whether the activity of SXR was ligand-dependent, mixtures of natural and synthetic compounds were tested for their ability to activate SXR in
20   transfection-based assays (see Example 3). A mixture containing dehydroepiandrosterone (DHEA) and pregnenolone was observed to be active, suggesting that SXR might be a new steroid receptor. To characterize its response properties, a large variety of steroids, including intermediate and major products of known steroid biosynthetic pathways were tested. Surprisingly, most of these
25   compounds were active, although there were clear differences in potency (see Figure 2). Indeed, most of the more than 70 steroids tested showed some activity at high doses. Activation was dependent on the ligand binding domain of SXR since both full-length

receptors and GAL4-receptor ligand binding domain chimeras showed similar activity, whereas there was no activation of reporter gene expression in experiments with reporter alone or reporter plus GAL4 DNA-binding domain.

5   The most potent and efficacious activator of the numerous steroids tested is corticosterone. Estradiol and dihydrotestosterone are also remarkably effective activators while aldosterone and 1,25 dihydroxy vitamin D3 are inactive, even at 50 mM. Although ligands for the classical steroid receptors do show some overlap in receptor specificity, there is no example of a nuclear receptor that can be activated by so many different types of steroids. This broad ligand specificity of SXR parallels that of

10   PPARα, which can be activated by an extremely diverse group of dietary fatty acids at micromolar levels (see, for example, Forman et al., in *Proc. Natl. Acad. Sci. USA* 94:4312 (1997) and Gottlicher et al., in *Proc. Natl. Acad. Sci. USA* 89:4653 (1992)).

        The diversity of steroids showing activity on SXR suggests that this novel class of receptors might be able to sense cumulative, as well as individual steroid levels,

15   predicting that combinations of activators might be more active than the individual components. As shown in Figure 3, a cocktail containing 10 steroids, each at 10 mM concentration (i.e., an overall steroid concentration of 100 mM), was considerably more active than its individual components at 10 mM, a concentration at which most were inactive. These results confirm that SXR is a broad-specificity, low-affinity, steroid-

20   activated receptor.

        An important requirement for physiologic homeostasis is the removal and detoxification of various endogenous hormones and xenobiotic compounds with biological activity. Much of the detoxification is performed by cytochrome P450 enzymes, many of which have broad substrate specificity and are inducible by a

25   bewildering array of compounds, including steroids. The ingestion of dietary steroids and lipids induces the same enzymes and thus, must be integrated into a coordinated metabolic pathway. Instead of possessing hundreds of receptors, one for each inducing

compound, the class of receptors described herein indicates the existence of a class of broad-specificity, low-affinity nuclear receptors that monitor total steroid levels and induce the expression of genes encoding xenobiotic metabolizing enzymes. These results indicate the existence of a steroid sensor mechanism for removal of elevated

5   levels of steroids (or steroid-like compounds) from circulation via broad-specificity, low-affinity receptors which represent a novel branch of the nuclear receptor superfamily.

Indeed, a search of the GENBANK database for genes containing putative SXR response elements identified a number of steroid hydroxylases, e.g., CYP2A1, CYP2A2,

10   CYP2C1, CYP2C6, CYP3A1, CYP3A2, P450 oxidoreductase and UDP-glucuronosyltransferase, as candidate target genes. The relevant portions of these sequences are as follows:

DR-3

rCYP3A1   tagac AGTTCA tga AGTTCA tctac (SEQ ID NO:3)

15   rCYP3A2   taagc AGTTCA taa AGTTCA tctac (SEQ ID NO:4)

rUGT1A6   actgt AGTTCA taa AGTTCA catgg (SEQ ID NO:5)

DR-4

rbCYP2C1   caatc AGTTCA acag GGTTCA ccaat (SEQ ID NO:6)

rP450R   cac AGGTGA gctg AGGCCA gcagc AGGTCG aaa (SEQ ID

20   NO:7)

DR-5

rCYP2A1   gtgca GGTTCA actgg AGGTCA acatg (SEQ ID NO:8)

rCYP2A2   gtgct GGTTCA actgg AGGTCA gtatg (SEQ ID NO:9)

rCYP2C6   agtct AGTTCA gtggg GGTTCA gtctt (SEQ ID NO:10)

25   hCYP2E1   gagat GGTTCA aggaa GGGTCA ttaac (SEQ ID NO:11)

The data shown in Figure 4 verify that SXR can activate DR-3, DR-4 and DR-5 elements that are present in these genes. In the series of transfections described in Example 3, corticosterone along with pregnenolone, progesterone, DHT, estradiol and

PCN are consistently among the best activators. Dexamethasone, cortisone and DHEA are in the intermediate group with little response from either aldosterone or cortisol (see Figure 4). Consistent with the DNA-binding data, maximal activities are achieved on βDR-3, βDR-4 and βDR-5 elements.

5   Thus, SXR response elements are found in genes encoding steroid hydroxylases, P450 oxidoreductase, and glucuronosyl transferase. These enzymes can metabolize endogenous as well as xenobiotic compounds and are legitimate targets for a receptor that is activated by pharmacological levels of steroids. SXR is highly expressed in liver, the major expression site of xenobiotic metabolizing enzymes, suggesting that the

10   steroid sensor mechanism is active in the appropriate tissue. In addition, prominent expression is also found in the intestine. Although less is known about the role of this tissue in steroid or xenobiotic metabolism, it is certainly possible that the intestine plays a role in regulating the metabolism of dietary, and perhaps endogenous, steroids. Taken together, these data strongly support the existence of a class of low-affinity, broad-

15   specificity nuclear hormone receptor(s), such as SXR, which function as intracellular "steroid sensor(s)".

          The localization of apparent SXR-responsive elements in genes encoding steroid hydroxylases raises the question of whether products of steroid catabolism, such as reduced or hydroxylated corticosterone derivatives, could also activate SXR. Figure 5

20   shows that both 5α and 5β reduced forms of corticosterone are effective SXR activators whereas 5α is slightly active and 5β is completely inactive on GR. While a few 5α-reduced steroids remain active (e.g., dihydrotestosterone), virtually all 5β-reduced steroids are unable to activate classical steroid receptors (see Russell and Wilson in *Ann. Rev. Biochem.* 63:25 (1994)). Accordingly, the activation of SXR by 5β-reduced

25   steroids reveals a previously unidentified role for these compounds in gene regulation.

          6β-hydroxy corticosterone is virtually inactive on SXR and slightly active on GR (see Figure 5). CYP3A genes, which contain SXR-activatable response elements,

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catalyze the hydroxylation of many steroids at the 6 position. Therefore, the inability of 6β-hydroxy-corticosterone to activate SXR suggests that 6-hydroxylation is a potential regulatory step in the SXR signaling pathway.

5 Thus, in support of the role for members of the SXR class of nuclear receptors proposed herein, it has been demonstrated herein that SXR is activated by an extremely diverse group of steroids and their metabolites, including molecules that have high-affinity receptors such as progesterone, testosterone, estrogen and corticosterone as well as their reduced catabolites that are, for the most part, inactive on the high-affinity receptors. In addition to the natural steroids, SXR is activated by synthetic steroids

10 including PCN and dexamethasone. These data provide a molecular explanation for the paradoxical induction of the CYP3A genes (a.k.a. P450$_{PCN}$) by both glucocorticoid receptor agonists and antagonists since the cyp3A genes harbor a SXR-activatable response element in the promoter region that has been shown to be responsible for PCN and glucocorticoid induction (see Burger et al. supra and Gonzalez et al. supra).

15 Whereas such a result is unexplainable by regulation of traditional, high-affinity steroid receptors, such behavior is consistent with the observed properties of the newly characterized steroid X receptor.

Further tests were conducted to discover whether P450s known to be inducible by PCN and other steroids could be SXR targets. The primary human steroid-

20 inducible P450 is the CYP3A4 gene (Molowa et al., *Proc. Natl. Acad. Sci. (USA)* 83:5311-5315, 1986, Beaune et al., *Proc. Natl. Acad. Sci. (USA)* 83:8064-8068, 1986). Unlike the rat and mouse CYP3A genes, all of which contain a DR-3 response element that SXR can activate (Figure 4), the human and rabbit promoters do not contain such an element. Inducibility of CYP3A4 by steroids and xenobiotics has

25 been localized to an 19 base pair element that is functional in transient transfection assays (Barwick et al., *Mol. Pharmacol.* 50:10-16, 1996). This element contains the IR-6 motif (TGAACTcaaaggAGGTCA) (SEQ ID NO:24). Similar elements have been identified in human CYP3A5, and CYP3A7 and in rabbit CYP3A6 genes

(Figure 6B) (Barwick, *supra*, 1996). Tests conducted to determine the ability of SXR to bind a series of inverted repeat elements with spacings from zero to six nucleotides determined that only an IR-6 response element, showed significant binding. As with the direct repeats, these results indicate the binding was dependent on formation of a

5 RXR:SXR heterodimer. In addition, competition binding experiments demonstrated little difference in the apparent affinity of SXR:RXR heterodimers for the βDR-4 and CYP3A4 IR-6 response elements. In accord with the known inducibility of the parent promoters, SXR was shown to activate reporter constructs containing the CYP3A4, but not the CYP3A5 or CYP3A7 motifs.

10 Compounds known to induce CYP3A4 were also shown to activate the invention SXR. The compounds tested included drugs, such as rifampicin and nifedipine; steroid antagonists, such as tamoxifen, spironolactone and PCN; natural and synthetic steroids, such as dexamethasone, diethylstilbestrol, estradiol, dihydrotestosterone, corticosterone and cortisone; and phytoestrogens, such as

15 coumestrol, equol and genistein. Of these compounds, rifampicin, nifedipine, corticosterone, estradiol, DES, and coumestrol were the most potent activators (Figure 7A. The mouse receptor PXR responded poorly to these inducers, but was preferentially activated by PCN, a weak activator of SXR (Figure 7B). PXR is reported to be preferentially activated by pregnanes (21-carbon steroids such as

20 dexamethasone (DEX) and pregnenolone) (Kliewer, *supra*, 1998); however, our tests showed that PXR is similarly activated by 19-carbon androstanes, like testosterone, and 18-carbon estranes, like estradiol (Figure 7B). Similar results were obtained with other natural steroids, including progesterone, pregnenolone and dihydroethanoic acid (DHEA).

25 To demonstrate that the activation of SXR and PXR by high steroid concentrations is not a general property of all steroid receptors, parallel tests were conducted to determine the activation of the human estrogen receptor (ER) by the same panel of compounds. The only endogenous steroids tested that activated the ER

were DHT and estradiol. The synthetic ER agonist, DES, and the phytoestrogens, including coumestrol (Figure 7C), also activated the human estrogen receptor.

Because the invention SXR-responsive elements are localized in genes encoding steroid hydroxylases, products of steroid catabolism, such as reduced or

5   hydroxylated corticosterone derivatives, were tested for activation of SXR. The results of these tests shown in Figure 7D illustrate that both 5α and 5β reduced forms of corticosterone are effective SXR activators; however, 5α is slightly active, and 5β is completely inactive on GR. While a few 5α-reduced steroids remain active (e.g., dihydrotestosterone), 5β-reduced steroids fail to activate classical steroid receptors

10   (Russell and Wilson, *Ann. Rev. Biochem.* 63:25-61. 1994). Therefore, the activation of SXR by 5β-reduced steroids may reflect a previously undetected regulatory pathway for these compounds. In addition, the virtual inactivity of, 6β-hydroxy corticosterone on SXR (Figure 6D), suggests that CYP3A4 catalyzed hydroxylation is a potential definitive regulatory step in steroid metabolism.

15   These results indicate that the induction of some xenobiotic-metabolizing enzymes by pharmacological levels of steroids, drugs, and xenobiotic compounds is regulated by a broad-specificity sensor, rather than numerous specific receptors. SXR is a novel member of the nuclear receptor superfamily that is activated by a diverse group of steroids and their metabolites. Direct regulation by a broad-specificity

20   sensor, such as the invention SXR, is biologically economical since much of the detoxification and catabolism of such compounds is mediated by cytochrome P450 enzymes, particularly members of the CYP3A family, which both metabolize, and are induced by, a wide spectrum of diverse compounds, including steroids.

Based on the above-described studies, a number of relationships have been

25   discovered among target genes, the SXR, and its activators that support the role of the SXR as a broad sensitivity sensor responsible for regulating cumulative levels of steroids and xenobiotics. First, SXR is expressed in tissues which catabolize steroids

and xenobiotics, particularly in liver, the major expression site of steroid and xenobiotic metabolizing enzymes, and in the intestine. Although less is known about the role of gut tissue in steroid metabolism, the gut is known to play an important role in first pass metabolism of dietary, and orally-administered compounds (Holtbecker et

5 al., *Drug Metab. Dispos.* 24:1121-1123, 1996; and Kolars et al., *Lancet* 338:1488-1490, 1991). For example, CYP3A4 is highly expressed in enterocytes (Kolars et al., *J. Clin. Invest.* 90:1871-1878, 1992). Thus, SXR is expressed at high levels in two key tissues for steroid and xenobiotic catabolism. Second, catabolic enzymes expressed in tissues that express SXR are induced by the invention SXR. SXR

10 response elements have been discovered in the well-characterized CYP3A4 promoter as well as those of P450 oxidoreductase, CYP2A, CYP2C, CYP2E and glucuronosyl transferase, which are all known to be involved in steroid and xenobiotic catabolism (F.J. Gonzalez, *Trends Pharmacol. Sci.* 13:346-352, 1992). Third, compounds known to induce catabolic enzymes activate the invention SXR, including drugs (such as

15 rifampicin and nifedipine), steroid receptor agonists and antagonists (such as estrogen and tamoxifen); bioactive dietary compounds (such as phytoestrogens), and the like. In particular, CYP3A4 is known to be inducible (Rendic and Di Carlo, 1997) by virtually all the compounds applicants have identified as SXR activators. Lastly, products of early catabolic steps, such as reduced steroids, activate SXR, ensuring

20 their complete inactivation and elimination. Taken together, these relationships support the role of the SXR as a broad-specificity sensor operative to regulate homeostasis of steroids and xenobiotics.

Activation of SXR also provides a molecular explanation for the paradoxical induction of the CYP3A genes (a.k.a. P450$_{PCN}$) by both glucocorticoid receptor

25 agonists and antagonists and for the differential response of orthologous enzymes in different species. The inducible CYP3A genes harbor response element in their promoters that has been shown to be responsible for PCN and glucocorticoid induction (Barwick, *supra*, 1996; Burger, supra, 1992; Gonzalez, supra, 1986; Schuetz and Guzelian, *supra*, 1984; and Kliewer, *supra*, 1998). Applicants have discovered

that these response elements can be activated by the invention SXR (Figures 6A and 6C). Despite their common role in steroid and xenobiotic catabolism, CYP3A genes from different species, and particularly the glucocorticoid-responsive promoter elements, show considerable differences in the pharmacology of their inducers

5   (Barwick, *supra*, 1996). For example, PCN is a strong inducer of rat CYP3A2 and CYP3A3, but a weak inducer of human CYP3A4 and rabbit CYP3A6. On the other hand, rifampicin is a strong inducer of the human and rabbit genes encoding such enzymes but not the rat genes (Barwick, *supra*, 1996).

However, when the response elements from such genes are tested by transient

10   transfection into primary hepatocytes from rats or rabbits, the responsiveness changes to that of the host cell type. For example, glucocorticoid-responsive elements from the rat CYP3A2 and CYP3A3 promoters were induced by DEX in both rat and rabbit hepatocytes, by PCN only in rat hepatocytes, and by rifampicin only in rabbit hepatocytes (Barwick, *supra*, 1996). Similarly, the glucocorticoid-responsive element

15   from the human CYP3A4 promoter was inducible by DEX in both rat and rabbit hepatocytes, by PCN only in rat hepatocytes, and by rifampicin only in rabbit hepatocytes (Barwick, *supra*, 1996). The activation profiles in rat cells correspond to the responsiveness of PXR to the inducers (Figure 6C); whereas the responsiveness in rabbit cells corresponds to that of SXR. Since the rabbit 3A6 promoter lacks the

20   rodent DR-3 element, but has the human IR-6 element (Barwick, *supra*, 1996), it can be inferred that rabbit liver will likely have a receptor more closely related to SXR than to PXR. Thus, the pharmacology of SXR and PXR activation explains the different inducibility of the rat, rabbit, and human members of the cytochrome P4503A family. This discovery suggests that rabbit hepatocytes behave more like

25   their human counterparts than do rodent hepatocytes, and that rabbits are perhaps better suited to testing for human-like drug interaction than rodents.

One additional member of the new branch of the nuclear receptor superfamily called the steroid and xenobiotic receptor has been discovered in mouse tissue.

Screening of a mouse liver cDNA library at reduced stringency resulted in the identification of 39 cDNAs, all of which encoded PXR.1. Orthologous nuclear receptors typically share greater than 90% amino acid identity in the ligand binding domain when comparing rodent and human receptors (e.g., RARα - 98%

5   human/mouse (h/m), PPARγ - 98% h/m, GR - 95% h/m, TRβ - 98% h/rat, ERα - 89% h/m). Therefore, PXR and SXR may represent α and β subtypes of the steroid and xenobiotic nuclear receptor family. This conclusion is supported by the distinct pharmacological properties of the receptors, as illustrated in the Examples herein. Further screening of mouse and human liver cDNA libraries has failed to identify

10   other family members. It is also possible that PXR and SXR represent unusually divergent orthologous genes. If this were correct, the divergence might reflect adaptation of the receptor to the difference between the diets of rodents and primates and the requirement for the receptor to respond to appropriate food-borne compounds.

To obtain the invention receptor, commercially obtained Northern blots of

15   multiple human tissues were probed by full-length SXR cDNA (SEQ ID NO: 1), as described in Example 1 herein. The results showed that SXR mRNA is expressed at high levels in human liver and at more moderate levels in human intestine. Exposures of the Northern blots for longer than 24 hours did not reveal expression in any other tissues. Multiple mRNAs were detected, ranging from 3500 nt to larger than 9000 nt.

20   Comparison of the sequences of the four cDNAs obtained reveals shared protein coding and 5' untranslated sequences, but a different 3' end for each of the four. These sequence differences may be due to alternative polyadenylation.

Electrophoretic mobility shift assays were employed to determine the ability of SXR to heterodimerize with RXR and to analyze the selectivity and specificity of

25   SXR DNA binding as described in Example 4 herein. Receptors that heterodimerize with RXR typically bind to direct repeats of AGGTCA or closely related sequences (Mangelsdorf and Evans, supra, 1995). SXR alone and in combination with RXR was tested against a series of response elements differing in the spacing between half

sites from 0 to 15 nucleotides. No binding was seen on classic steroid response elements. In contrast, strong binding was selective to a DR-4 motif with minimal binding to DR-3 and DR-5, and no binding to other spacings. When the variant AGTTCA (βDR) half site was used, strong binding was seen on βDR-4 and βDR-5, and significant, but reduced, binding to βDR-3. These results demonstrate that SXR binds DNA as a heterodimer with RXR rather than as a homodimer like the classical steroid receptors (Beato, *supra*, 1995).

To determine whether the activity of SXR was ligand-dependent, mixtures of natural and synthetic compounds were tested for their ability to activate SXR in transfection-based assays. A mixture containing DHEA and pregnenolone was active, suggesting that SXR might be a new steroid receptor. To characterize more fully the response properties of the receptors, a large variety of steroids, including intermediate metabolites and major products of known steroid biosynthetic pathways were tested for ability to activate the invention SXR. As illustrated by the results shown in Figure 2, most of these compounds were active, although there were clear differences in potency. Of the more than 70 steroids tested, most showed some activity at high doses. It was also discovered that both full-length receptors and GAL4-receptor ligand binding domain chimeras showed similar activity; but no activation of reporter gene expression was detected in experiments with reporter alone or reporter plus GAL4 DNA-binding domain (Figure 2). These results indicate that activation is dependent on the ligand-binding domain of SXR.

The most potent and efficacious activator of the numerous steroids tested was corticosterone (Figure 2). Estradiol and dihydrotestosterone were also remarkably effective activators, while aldosterone and 1,25 dihydroxy vitamin D3 were inactive, even at a concentration of 50 μM (Figure 2). Although ligands for the classical steroid receptors do show some overlap in receptor specificity, there is no known example of a nuclear receptor that can be activated by so many different types of steroids. This broad ligand specificity of the invention SXR parallels that of PPARα,

which is activated by a very diverse group of dietary fatty acids at micromolar levels
(Forman et al., *Proc. Natl. Acad. Sci. USA* 94:4312-4317, 1997; Gottlicher et al.,
Proc. Natl. Acad. Sci. USA 89:4653-4657, 1992; Kliewer et al., *Proc. Natl. Acad. Sci.
(USA)* 94:4318-4323, 1997).

5   A search of the GENBANK database for genes containing potential SXR
response elements identified the steroid hydroxylases CYP2A1, CYP2A2, CYP2C1,
CYP2C6, CYP3A1, CYP3A2, P450 oxidoreductase, and UDP-glucuronosyl-
transferase as candidate target genes (Figure 6A). The search identified DR-3, DR-4
and DR-5 elements present in these genes, which indicates that such compounds
10   activate the invention SXR. Similarly, the transfection-based assays described in
Example 4, which were conducted to test the ability of steroids and xenobiotics to
activate SXR response elements showed that corticosterone along with pregnenolone,
progesterone, dihydrotestosterone (DHT), estradiol, and PCN are consistently among
the best activators. Dexamethasone, cortisone, and DHEA are in the group of
15   intermediate activators, and there is little response from either aldosterone or cortisol
(Figure 4). Consistent with the DNA-binding data, maximal activities induced by
these activators was achieved in steroid inducible P450 genes containing βDR-3,
βDR-4, and βDR-5 response elements (Figure 4)

          The term "effective amount" as applied to a SXR polypeptide agonist or
20   antagonist according to the invention means the quantity necessary to modulate
metabolism of one or more steroid and/or xenobiotic compounds to a desired level, for
example, a level effective to treat, cure, or alleviate the symptoms of a disease state
for which the therapeutic compound is being administered, or to establish
homeostasis. Alternatively, when an agonist according to the invention is employed to
25   prevent steroid toxicity in a subject therapeutically administered one or more therapeutic
steroid and/or xenobiotic compounds in treatment of a disease state, the term "effective
amount" is an amount necessary to bring the overall level of steroids and xenobiotic
compounds to a safe level, for example as determined by blood tests of the individual

being treated for the effects of steroid toxicity, or to alleviate the symptoms of steroid toxicity as determined by the physician. Similarly, the amount of a SXR polypeptide antagonist according to the invention used to slow clearance of a therapeutic steroid or xenobiotic compound is an amount necessary to raise the blood level of the particular

5   therapeutic compound to a therapeutic level and hence treat or alleviate the symptoms of the disease state for which the therapeutic steroid or xenobiotic compound is being administered. Since individual subjects may present a wide variation in severity of symptoms and each drug or active agent has its unique therapeutic characteristics, the precise mode of administration, dosage employed and treatment protocol for each

10   subject is left to the discretion of the practitioner.

Amounts effective for the particular therapeutic goal sought will, of course, depend on the severity of the condition being treated, and the weight and general state of the subject. Various general considerations taken into account in determining the "effective amount" are known to those of skill in the art and are described, e.g., in

15   Gilman et al., eds., Goodman And Gilman's: The Pharmacological Bases of Therapeutics, 8th ed., Pergamon Press, 1990; and Remington's Pharmaceutical Sciences, 17th ed., Mack Publishing Co., Easton, Pa., 1990, each of which is herein incorporated by reference.

Pharmaceutical formulations of the SXR polypeptide agonists or antagonists of

20   the present invention can be used in the form of a solid, a solution, an emulsion, a dispersion, a micelle, a liposome, and the like, wherein the resulting formulation contains one or more of the agonists or antagonists contemplated for use in the practice of the present invention, as active ingredients, in admixture with an organic or inorganic carrier or excipient suitable for enteral or parenteral applications. The active ingredients

25   may be compounded, for example, with the usual non-toxic, pharmaceutically acceptable carriers for tablets, pellets, capsules, suppositories, solutions, emulsions, suspensions, and any other form suitable for use. The carriers which can be used include glucose, lactose, gum acacia, gelatin, mannitol, starch paste, magnesium

trisilicate, talc, corn starch, keratin, colloidal silica, potato starch, urea, medium chain length triglycerides, dextrans, and other carriers suitable for use in manufacturing preparations, in solid, semisolid, or liquid form. In addition auxiliary, stabilizing, thickening and coloring agents and perfumes may be used. The active compounds (i.e.,

5   one or more SXR polypeptide agonist or antagonist) are included in the pharmaceutical formulation in an amount sufficient to produce the desired effect upon the target process, condition or disease.

Pharmaceutical formulations containing the active ingredients contemplated herein may be in a form suitable for oral use, for example, as tablets, troches, lozenges,

10   aqueous or oily suspensions, dispersible powders or granules, emulsions, hard or soft capsules, or syrups or elixirs. Formulations intended for oral use may be prepared according to any method known in the art for the manufacture of pharmaceutical formulations. In addition, such formulations may contain one or more agents selected from a sweetening agent (such as sucrose, lactose, or saccharin), flavoring agents (such

15   as peppermint, oil of wintergreen or cherry), coloring agents and preserving agents, and the like, in order to provide pharmaceutically elegant and palatable preparations. Tablets containing the active ingredients in admixture with non-toxic pharmaceutically acceptable excipients may also be manufactured by known methods. The excipients used may be, for example, (1) inert diluents such as calcium carbonate, lactose, calcium

20   phosphate, sodium phosphate, and the like; (2) granulating and disintegrating agents such as corn starch, potato starch, alginic acid, and the like; (3) binding agents such as gum tragacanth, corn starch, gelatin, acacia, and the like; and (4) lubricating agents such as magnesium stearate, stearic acid, talc, and the like. The tablets may be uncoated or they may be coated by known techniques to delay disintegration and absorption in the

25   gastrointestinal tract, thereby providing sustained action over a longer period. For example, a time delay material such as glyceryl monostearate or glyceryl distearate may be employed. They may also be coated by the techniques described in the U.S. Patent Nos. 4,256,108; 4,160,452; and 4,265,874, to form osmotic therapeutic tablets for controlled release.

In some cases, formulations for oral use may be in the form of hard gelatin capsules wherein the active ingredients are mixed with an inert solid diluent, for example, calcium carbonate, calcium phosphate, kaolin, or the like. They may also be in the form of soft gelatin capsules wherein the active ingredients are mixed with water

5   or an oil medium, for example, peanut oil, liquid paraffin, or olive oil.

The pharmaceutical formulations may also be in the form of a sterile injectable solution or suspension. This suspension may be formulated according to known methods using suitable dispersing or wetting agents and suspending agents. The sterile injectable preparation may also be a sterile injectable solution or suspension in a non-

10   toxic parenterally-acceptable diluent or solvent, for example, as a solution in 1,4-butanediol. Sterile, fixed oils are conventionally employed as a solvent or suspending medium. For this purpose any bland fixed oil may be employed including synthetic mono- or diglycerides, fatty acids (including oleic acid), naturally occurring vegetable oils like sesame oil, coconut oil, peanut oil, cottonseed oil, or synthetic fatty vehicles,

15   like ethyl oleate, or the like. Buffers, preservatives, antioxidants, and the like, can be incorporated as required.

Formulations contemplated for use in the practice of the present invention may also be administered in the form of suppositories for rectal administration of the active ingredients. These formulations may be prepared by mixing the active ingredients with

20   a suitable non-irritating excipient, such as cocoa butter, synthetic glyceride esters of polyethylene glycols (which are solid at ordinary temperatures, but liquify and/or dissolve in the rectal cavity to release the active ingredients), and the like.

The invention will now be described in greater detail by reference to the following non-limiting examples.

Example 1

cDNA identification

SXR was identified from a human genomic library (Clontech) hybridized with a full-length cDNA encoding Xenopus BXR (Blumberg et al., 1998a) under reduced
5   stringency conditions (hybridization in 0.5 M $NaPO_4$ pH 7.0, 7% sodium dodecyl sulfate (SDS), 5% dextran sulfate at 65° C overnight, washing three times twenty minutes in 2 x standard saline citrate solution (0.15M saline containing 0.015M sodium citrate, pH 7) (SSC), 0.1% SDS at 37° C). Restriction mapping and Southern blot analysis showed that three exons were contained within the 9 kb EcoRI
10   hybridizing fragment. This fragment was used to probe a Northern blot of multiple types of human tissue (Clontech) at high stringency (hybridization as above, washing twice for 20 minutes in 0.1x SSC, 0.1% SDS at 50° C) and hybridization was detected in liver. A human liver cDNA library (Stratagene, La Jolla, CA) was subsequently screened using the same conditions, and four independent clones were identified.
15   Each of these clones was sequenced on both strands within the protein coding region. DNA sequences were compiled and aligned using the programs of Staden (R. Staden, *Nucl. Acids Res.* 14:217-231, 1986), University of Wisconsin Genetics Computer Group (Devereaux et al., *Nucl. Acids Res.* 12:387-395, 1984). Database searching was performed using the BLAST network server at the National Center for
20   Biotechnology Information (Altschul et al., *J. Mol. Biol.* 215:403-410, 1990). PXR was isolated from a mouse liver cDNA library (Stratagene) by screening with the SXR protein coding region at reduced stringency (5xSSC, 43% formamide, 5x Denhardts, 0.1% SDS, 0.1 mg/ml denatured, sonicated salmon sperm DNA at 37° C). Three, twenty minute washes were performed in 0.5 x SSC, 0.1% SDS at 50° C.

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Example 2

Ability of SXR to heterodimerize with RXR

The protein coding region of SXR was PCR amplified and subcloned into
NcoI and BamHI sites of the vector pCDG1 (Blumberg, *supra*, 1998a) using ExoIII-
mediated ligation independent cloning (Li and Evans, *Nucl. Acids Res.* 25, 4165-4166,
1997). During this process the putative initiator Leu was converted to Met with a
Kozak consensus sequence CCATGG. The actual response elements and the number
of copies are as follows: the base vector is tk-luc in all cases (Hollenberg et al., *Nature*
318:635-641, 1985):

DR-1, tk(ApoAI)$_4$ (Ladias and Karathanasis, *Science* 251:561-565, 1991);

DR-2, tk(Hox-B1-RARE)$_2$ (Ogura and Evans, *Proc. Natl. Acad. Sci. (USA)*
92:387-391, 1995);

βDR-3, tk(CYP3A2)$_3$ (Kliewer et al., *Cell* 92:73-82, 1998),

DR-4, tk(MLV-TRE)$_2$ (Umesono et al., *Cell* 65:1255-1266, 1991);

βDR-4, tk(LXRE)$_3$ (Willy et al., *Genes Dev.* 9:1033-1045, 1995);

βDR-5, tk(βRARE)$_3$ (Sucov et al., *Proc. Natl. Acad. Sci. (U.S.A.)* 87:5392-
5396, 1990);

TRE$_p$, tk(TRE$_p$)$_2$ (Umesono et al., *supra*, 1991).

Direct repeat 0-15 (DR-0 up to DR-15) oligonucleotides employed herein had
the following sequences:

DR-0: catagtc AGGTCA AGGTCA gatcaac (SEQ ID NO:12);

DR-1: catagtc AGGTCA t AGGTCA gatcaac (SEQ ID NO:13);

DR-2: catagtc AGGTCA at AGGTCA gatcaac (SEQ ID NO:14);

DR-3: catagtc AGGTCA tat AGGTCA gatcaac (SEQ ID NO:15);

DR-4: catagtc AGGTCA tata AGGTCA gatcaac (SEQ ID NO:16);

DR-5: catagtc AGGTCA tatat AGGTCA gatcaac (SEQ ID NO:17);

DR-6: catagtc AGGTCA tatata AGGTCA agatcaac (SEQ ID NO:18);

DR-7: catagtc AGGTCA tatatat AGGTCA gatcaac (SEQ ID NO:19);

DR-10: catagtc AGGTCA tatatatata AGGTCA gatcaac (SEQ ID NO:20);

DR-15: catagtc AGGTCA tagtagtagtagtag AGGTCA gatcaac (SEQ ID NO:21).

GAL4-SXR was constructed by subcloning aa 107-434 of SEQ ID NO:2 into pCMX-GAL4 (Perlmann, *supra*, 1993).

5   Similarly, the PXR.1 protein coding region was PCR amplified and subcloned into a NcoI-BamHI cut in pCDG1, while amino acids 104 to 431 were subcloned into CMX-GAL4. Reporter plasmids were constructed by synthesizing three-copy response elements and subcloning into a HindIII-BamHI cut in pTk-luc (Hollenberg et al., *Cell* 49:39-46, 1987).

10   CV-1 cells were maintained in Dulbecco's Modified Eagle's Medicine (DMEM) containing 10% resin-charcoal stripped calf bovine serum (CBS). Liposome-mediated transient transfections were performed using 1,2-bis(oleoyloxy)-3-(trimethylammonio) propane (DOTAP) reagent (Boehringer Manheim) at a concentration of 5 μg/ml in DMEM containing 10% resin charcoal stripped fetal

15 bovine serum in 96-well format using a Beckman Biomek 1000 laboratory workstation as described in (Blumberg et al., *Proc. Natl. Acad. Sci. (USA)* 93:4873-4878, 1996). Test ligands were added the next day in DMEM containing 10% delipidated fetal bovine serum (FBS). After 18-24 hours incubation, the cells were lysed and luciferase reporter gene assays and β-galactosidase transfection control

20 assays were performed as described in (Blumberg, *supra*, 1996). Reporter gene expression was normalized to the β-galactosidase transfection control and expressed as relative light units per optical density unit per minute of β-galactosidase activity, or fold induction over solvent control. Each data point represents the average of triplicate experiments +/- standard error and was replicated in independent

25 experiments.

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Example 3

Cell culture and transfection studies

To determine whether the activity of SXR was ligand-dependent, mixtures of natural and synthetic compounds were tested for their ability to activate SXR in

5   transfection-based assays. Thus, the protein coding region of SXR was PCR amplified and subcloned into NcoI and BamH1 sites of the vector pCDG1 (see Blumberg et al., supra). During this process the putative initiator Leu was converted to Met with a Kozak consensus sequence CCATGG.

GAL4-SXR was constructed by cloning amino acid residues 134-446 of SXR

10   into pCMX-GAL4 (see Perlman et al. supra). CV-1 cells were maintained in DMEM containing 10% resin-charcoal stripped calf bovine serum. Liposome-mediated transient transfections were performed using DOTAP reagent (Boehringer Manheim) at a concentration of 5 mg/ml in DMEM containing 10% resin charcoal stripped fetal bovine serum in 96-well format using a Beckman Biomek 1000 laboratory workstation

15   as previously described by Blumberg et al., in *Proc. Natl. Acad. Sci. (USA)* **93**:4873 (1996)).

Ligands were added the next day in DMEM containing 10% delipidated FBS. After 18-24 hours incubation, the cells were lysed and luciferase reporter gene assays and b-galactosidase transfection control assays performed as previously described by

20   Blumberg et al. (1996), supra. Reporter gene expression was normalized to the b-galactosidase transfection control and expressed as relative light units per O.D. per minute of b-galactosidase activity or fold induction over solvent control. Each data point (see Figure 2) represents the average of triplicate experiments +/- standard error and was replicated in independent experiments.

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Example 4

DNA-binding analysis

Electrophoretic mobility shift assays were performed using *in vitro*
transcribed, translated proteins (TNT, Promega). Proteins (1 μl each) were incubated
5   for 20 minutes at room temperature with 100,000 cpm of Klenow-labeled probes in 10
mM Tris pH 8, 100 mM KCl, 6% glycerol, 0.05% NP-40, 1 mM dithiothreitol (DTT),
100 ng/μl poly dI:dC (Pharmacia, Piscataway, NJ) and then electrophoresed through a
5% polyacrylamide gel in 0.5x TBE (45mM Tris-base, 45 mM boric acid, 1 mM
ethylenediaminetetraacetic acid (EDTA) at room temperature. For competition
10   binding, protein plus unlabeled oligonucleotides at five or fifty fold molar excess were
preincubated for ten minutes on ice, then labeled probes were added and incubated for
20 minutes at room temperature. Electrophoresis was as above. The IR series
oligonucleotides tested had the following sequences:

IR-0, agcttAGGTCATGACCTa (SEQ ID NO:25);
15   IR-1, agcttAGGTCAgTGACCTa (SEQ ID NO:26);
IR-2, agcttAGGTCAcgTGACCTa (SEQ ID NO:27);
IR-3, agcttAGGTCAcagTGACCTa, (SEQ ID NO:28
IR-4, agcttAGGTCAcatgTGACCTa (SEQ ID NO:29);
IR-5, agcttAGGTCAcactgTGACCTa (SEQ ID NO: 30);
20   IR-6, agcttTGAACTcaaaggAGGTCA) (SEQ ID NO:31); and
IR-M, agcttACGTCATGACGTa (SEQ ID NO:32).

Mutations in the IR-M nucleotide sequence prevented binding of the
heterodimer to the response element.

CYP3A oligonucleotides tested had the following sequences:
25   CYP3A4,tagaataTGAACTcaaaggAGGTCAgtgagtgg (SEQ ID NO:31);
CYP3A5, tagaataTGAACTcaaaggAGGTAAgcaaaggg (SEQ ID NO:32); and
CYP3A7, tagaataTTAACTcaatggAGGCAgtgagtgg (SEQ ID NO:33)

It will be apparent to those skilled in the art that various changes may be made in the invention without departing from the spirit and scope thereof, and therefore, the invention encompasses embodiments in addition to those specifically disclosed in the specification, but only as indicated in the appended claims.

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WE CLAIM:

1.   A receptor polypeptide, or functional fragments thereof, wherein said polypeptide is characterized by:

        forming a heterodimer with retinoid X receptor (RXR),

        binding to a direct or inverted repeat response element motif based on the half site AGTTCA,

        activating transcription through response elements found in steroid inducible P450 genes in response to a wide variety of natural and synthetic steroid hormones; and

        being prominently expressed in the liver and the intestine.

2.   A polypeptide according to Claim 1 wherein said polypeptide is further characterized by having a DNA binding domain of about 67 amino acids with 9 Cys residues, wherein said DNA binding domain has about 73 % amino acid identity with the DNA binding domain of the *Xenopus* benzoate X receptor.

3.   A polypeptide according to Claim 2 wherein said polypeptide is further characterized by having a ligand binding domain of about 198 amino acids, wherein said ligand binding domain has about 52 % amino acid identity with the ligand binding domain of the *Xenopus* benzoate X receptor.   __

4.   A polypeptide according to Claim 1, wherein said polypeptide has substantially the same amino acid sequence as shown in SEQ ID NO:2.

5.   A polypeptide according to Claim 1, wherein said polypeptide has the same amino acid sequence as shown in SEQ ID NO:2.

6.   A heterodimer complex consisting of RXR and SXR.

7.   Isolated nucleic acid which encodes a polypeptide according to Claim 1.

8.   Nucleic acid according to Claim 7 wherein said nucleic acid encodes substantially the same amino acid sequence as shown in SEQ ID NO:2.

9.   Nucleic acid according to Claim 7 wherein said nucleic acid encodes the same amino acid sequence as shown in SEQ ID NO:2.

10.   Nucleic acid according to Claim 7 comprising a segment having a contiguous nucleotide sequence which is substantially the same as nucleotides 583 - 1884 shown in SEQ ID NO:1.

11.   Nucleic acid according to Claim 7 comprising a segment having a contiguous nucleotide sequence which is the same as nucleotides 583 - 1884 shown in SEQ ID NO:1.

12.   A labeled single-stranded nucleic acid, comprising at least 20 contiguous bases in length having substantially the same sequence as any 20 or more contiguous bases selected from bases 1 - 2068, inclusive, of the DNA illustrated in SEQ ID NO:1, or the complement thereof.

13.   A nucleic acid according to Claim 12 which is labeled with ^{32}P.

14.   A nucleic acid according to claim 12 comprising at least 20 contiguous bases in length having substantially the same sequence as any 20 or more contiguous bases selected from bases 583 - 1884, inclusive, of the DNA illustrated in SEQ ID NO:1, or the complement thereof.

15.   An isolated nucleic acid construct comprising:
        (i)   the nucleic acid of Claim 7 operatively linked to
        (ii)   regulatory element(s) operative for transcription of said nucleic acid sequence and expression of said polypeptide in an animal cell in culture.

16.   An animal cell in culture which is transformed with a nucleic acid construct according to Claim 15.

17.   A cell according to Claim 16, wherein said cell is further transformed with a reporter vector which comprises:

5
        (a)   a promoter that is operable in said cell,

        (b)   a hormone response element, and

        (c)   DNA encoding a reporter protein,

                wherein said reporter protein-encoding DNA is operatively

        linked to said promoter for transcription of said DNA, and

10
                wherein said promoter is operatively linked to said hormone

        response element for activation thereof.

18.   An antibody which specifically binds a receptor polypeptide according to claim 1.

19.   An antibody according to claim 18 wherein said antibody is a

15   monoclonal antibody.

20.   A method of making a receptor polypeptide according to claim 1, said method comprising culturing cells containing an expression vector operable in said cells to express a DNA sequence encoding said polypeptide.

21.   A method of identifying a receptor polypeptide, or functional fragments thereof, wherein said polypeptide is characterized by:

forming a heterodimer with retinoid X receptor (RXR),

binding to a direct or inverted repeat response element motif based on the half site AGTTCA,

activating transcription through response elements found in steroid inducible P450 genes in response to a wide variety of natural and synthetic steroid hormones, and

being prominently expressed in the liver and the intestine,

said method comprising hybridizing test DNA with a probe according to claim 14 under high stringency conditions, and selecting those sequences which hybridize to said probe.

22.   A method for screening a collection of compounds to determine those compounds which bind to SXR, said method comprises employing the receptor of claim 1 in a binding assay.

23.   A method of testing a compound for its ability to regulate transcription-activating effects of a receptor polypeptide according to claim 1, said method comprising assaying for the presence or absence of reporter protein upon contacting of cells containing said receptor polypeptide and reporter vector with said compound:

wherein said reporter vector comprises:

(a)   a promoter that is operable in said cell,

(b)   a hormone response element, and

(c)   DNA encoding a reporter protein,

wherein said reporter protein-encoding DNA is operatively linked to said promoter for transcription of said DNA, and

wherein said promoter is operatively linked to said hormone response element for activation thereof.

24.   A method to identify compounds which are agonists of steroid X receptor (SXR), but do not agonize or antagonize other steroid receptors, said method comprising:

5   detecting in a first assay system the presence or absence of reporter protein upon contacting of cells containing SXR and reporter vector with said compound;

wherein said reporter vector comprises:

(a)   a promoter that is operable in said cell,

(b)   an SXR response element, and

10   (c)   DNA encoding a reporter protein,

wherein said reporter protein-encoding DNA is operatively linked to said promoter for transcription of said DNA, and

wherein said promoter is operatively linked to said SXR

15   response element for activation thereof;

detecting in a second assay system the presence or absence of reporter protein upon contacting of cells containing a steroid hormone receptor other than SXR and reporter vector with said compound;

wherein said reporter vector comprises:

20   (a)   a promoter that is operable in said cell,

(b)   a response element for said receptor other than $\overline{SXR}$, and

(c)   DNA encoding a reporter protein,   _

wherein said reporter protein-encoding DNA is operatively linked to said promoter for transcription of said

25   DNA, and

wherein said promoter is operatively linked to said response element for said receptor other than SXR for activation thereof; and

identifying those compounds which induce production of reporter in said

30   first assay, but not in said second assay, as compounds which are agonists of

54

steroid X receptor (SXR), but neither agonists nor antagonists of other steroid receptors.

25.   A method for modulating process(es) mediated by receptor polypeptides according to claim 1, said method comprising conducting said process(es) in the presence of at least one agonist, antagonist or antibody raised against said polypeptide.

26.   A method for inducing the expression of steroid degradative enzymes, said method comprising activating SXR.

27.   A method for modulating metabolism of one or more xenobiotic steroid and/or xenobiotic compound(s) in a subject in need thereof, said method comprising administering to the subject an effective amount of a modulator of a steroid and xenobiotic receptor (SXR) polypeptide that activates transcription of an endogenous gene operatively associated with a steroid and xenobiotic receptor (SXR) response element.

28.   The method according to claim 27 wherein the modulator is an agonist.

29.   The method according to claim 27 wherein the modulator is an antagonist.

30.   The method according to claim 27 wherein the gene encodes a member of the cytochrome P450 family.

31.   The method according to claim 27 wherein the steroid and/or xenobiotic compound is selected from the group consisting of a phytoestrogen, and a calcium channel blocker.

32.   A method for preventing steroid toxicity in a subject administered one or more therapeutic steroid and/or xenobiotic compounds for the treatment of a disease state, said method comprising administering to the subject an amount of an agonist for a SXR polypeptide to activate transcription of an endogenous gene operatively associated with a SXR response element effective to lower the overall level of steroids in the subject to a physiologically acceptable level.

33.   The method according to claim 32 wherein the gene encodes a member of the cytochrome P450 family.

34.   The method according to claim 32 wherein the therapeutic compound is a steroid.

35.   The method according to claim 34 wherein the disease state is tuberculosis.

36.   The method according to claim 35 wherein the therapeutic compound is rifampin, or an active derivative or analog thereof.

37.   The method according to claim 34 wherein the disease state is breast cancer.   ——

38.   The method according to claim 37 wherein the therapeutic compound is tamoxifen, raloxifene, or a derivative or analog thereof.

39.   The method according to claim 34 wherein the disease state is osteoporosis.

40.   The method according to claim 39 wherein the therapeutic compound is vitamin K.

41.   The method according to claim 41 wherein the therapeutic compound is propanolol.

42.   The method according to claim 32 wherein the therapeutic compound is a calcium channel blocker.

5   43.   The method according to claim 42 wherein the calcium channel blocker is nifedipine.

44.   A method for slowing clearance of a therapeutic steroid or xenobiotic compound from a subject in need thereof, said method comprising administering to the subject an effective amount of an antagonist for a SXR receptor polypeptide that 10   activates transcription of an endogenous gene operatively associated with a SXR response element.

45.   A screening assay for determining whether a test compound, or combinations thereof, activate a steroid and xenobiotic receptor (SXR) polypeptide, said assay comprising:

a)   contacting a host cell line containing a SXR polypeptide and a
5   reporter vector with one or more test compound(s) in an appropriate culture medium,

wherein the reporter vector comprises

1)   a promoter that is operable in the cell,

2)   a SXR response element, and

10   3)   DNA encoding a reporter protein operatively

linked to the promoter for transcription of the DNA,

wherein the promoter is operatively linked to the SXR response

element for activation thereof, and

(b)   determining the presence or absence of the reporter protein,
15   wherein the presence of the reporter protein indicates the test compound activates the SXR receptor polypeptide, and the absence of the reporter protein indicates the test compound does not activate the SXR receptor polypeptide.

46.   The assay according to claim 45 wherein the expression of the reporter compound in the assay indicates a greater than 30% likelihood that administration of
20   the test compound to a subject at a therapeutic level would cause a drug interaction of the test compound with other steroid and/or xenobiotic compounds in the subject.

47.   The assay according to claim 45 wherein the test compound is a combination of therapeutic steroid compounds and the level of expression of the reporter compound indicates the level of drug interaction between the therapeutic
25   compounds expected if the combination is coadministered to a subject.

48.   A method for treating a disease state in a subject in need thereof comprising administering to the subject an effective amount of steroid and/or xenobiotic compound(s) that modulates transcription of an endogenous SXR polypeptide in the subject.

5   49.   The method according to claim 48 wherein the compound is an agonist of the SXR polypeptide and the disease state is characterized by a higher level of an endogenous steroid than is consistent with homeostasis.

50.   The method according to claim 49 wherein the disease state is selected from the group consisting of Cushing's syndrome, virilism and hirsutism in females,

10   polycystic ovarian syndrome, 21-hydroxylase deficiency, 11β-hydroxylase deficiency, 3β-hydroxysteroid dehydrogenase deficiency, 17-hydroxylase deficiency, and breast, colorectal and prostate cancers.

51.   The method according to claim 48 wherein the compound is an antagonist of the SXR polypeptide and the disease state is characterized by a lower

15   level of an endogenous steroid than is consistent with homeostasis.

```
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181 AGAACAAATACGTAATCTCTTCATTGCTAGTTCAAGTGCTGGACTTAGGAGGGGCAATGGAGCCGCTTAGTGCCTACATCT

271 GACTTGGACTGAAATATAGGTGAGAGACAAGATTGTCTCATATCCGGGAAATCATAACCTATGACTAGGACGGGAAGAGAGGAAGCACTGC

361 CTTTACTTCAGTGGGAATCTCGGCCTCAGCCTGCAAGCCAAGTGTTCACAGTGAGAAAGCAAGAGAATAAGCTAATACTCCTGTCCTGA

451 ACAAGGCAGCGGCTCCTTGGTAAAGCTACTCCTTGATCGATCCTTTGCACCGGATTGTTCAAAGTGGACCCCAGGGGAGAAGTCGGAGCA

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631 TGTGAGGACACAGAGTCTGTTCCTGAAAGCCCAGTGTCAACGCAGATGAGGAAGTCGGAGTCCCCAAATCTGCCGTGTATGTGGGAC
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721 AAGGCCACTGGCTATCACTTCAATGTCATGACATGTGAAGGATGCAAGGGCtTTTTCAGGAGGGCCATGAAACGCAACGCCCGGCTGAGG
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811 TGCCCCTTCCGGAAGGGCGCCTGCGAGATCACCCGGAGGCAGTGCCAGGCCTGCCGCCTGCGGAAGTGCCTGGAGAGCGGC
    C  P  F  R  K  G  A  C  E  I  T  R  R  Q  C  Q  A  C  R  L  R  K  C  L  E  S  G   106

901 ATGAAGAAGGAGATGATCATGTCCGACGAGGCCGTGGAGGAGAGGCGGGCCCTTGATCAAGCGGAAGAAAGTGAACGGACAGGGACTCAG
    M  K  K  E  M  I  M  S  D  E  A  V  E  E  R  R  A  L  I  K  R  K  K  S  E  R  T  G  T  Q   136
```

FIGURE 1A-1

991 CCACTGGGAGTGCAGGGGCTGACAGAGGAGCAGCGGATGATGATCAGGGAGCTCAGATGAAAAACCTTTGACACTACTTC
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1081 TCCCATTTCAAGAATTCCGGCTGCCAGGGGTGCTTAGCAGTGGCTGCGAGTTGCCAGAGCCTCTGCAGCCCATGAGGAAGAAGCT
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1171 GCCAAGTGGAGCCAGTCCGGAAAGATCTGTGCTCTTCTTTGAAGGTCTCTGCAAGCTGCGGGGGAGGATGCCAGTGTCTGAACTACAA
      A K W S Q V R K D L C S L K V S L Q A A G G G W Q C L E L Q   226

1261 ACNCCCAGCCGACAGTGGCGGAAAGAGATCTTCTCCCTGCTCCCCCACATGGCTGACATGTCAACTACATGTTCAAAGGCATCATCAGC
      T P S R Q W R K E I F S L L P H M A D M S T Y M F K G I I S   256

1351 TTTGCCAAAGTCATCTCCTACTTCAGGGACTTGCCCATCGAGGACCAGATCTCCCTGCTGAAGGGGGCCGCTTTCGAGCTGTGTCAACTG
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1441 AGATTCAACACAGTGTTCAACGCGGAGACTGGAACCTGGGAGTGTGGCCGGCTGTCCTACTGCTTGGAAGACACTGCAGGTGGCTTCCAG
      R F N T V F N A E T G T W E C G R L S Y C L E D T A G G F Q   316

1531 CAACTTCTACTGGAGCCATGCTGAAATTCCACTACATGCTGAAGAAGCTGCAGCTGCATGAGGAGTATGTGCTGATGCAGGCCATC
      Q L L E P M L K F H Y M L K K L Q L H E E E Y V L M Q A I   346

1621 TCCCTCTTCTCCCCAGACCGGCCCAGGTGTGCTGCAGCACCGCGTGGTGGACCAGCTGCAGGAGCAATTCGCCATTACTCTGAAGTCCTAC
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1711 ATTGAATGCAATCGGCCCCCAGCCTGCTGCTAGGTTCTTGTTCCTGAAGATCATGGCTATGCTCACCGAGCTCCGCAGCATCAATGCTCAG
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1801 CACACCCAGCGGCTGCTGCGCATCCAGGACATACACCCCTTTGCTACGCCCCTCATGCAGGAGTTGTTCGGCATCACAGGTAGCTGAGCG
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FIGURE 1A-2
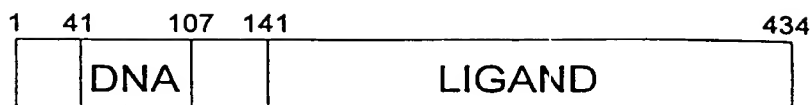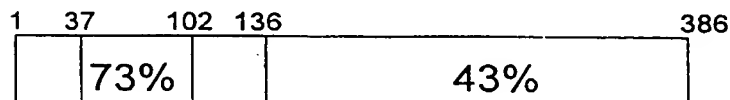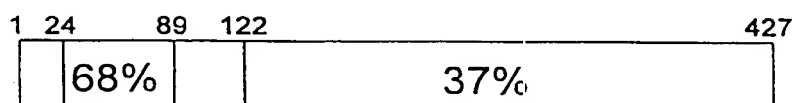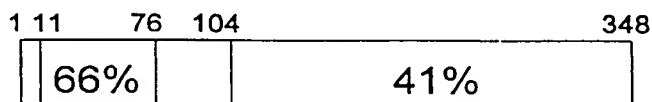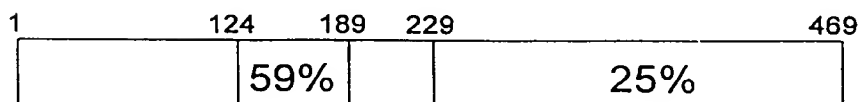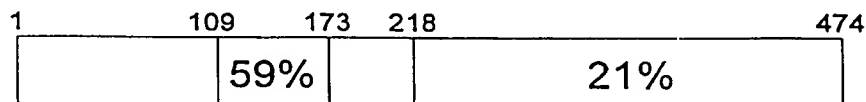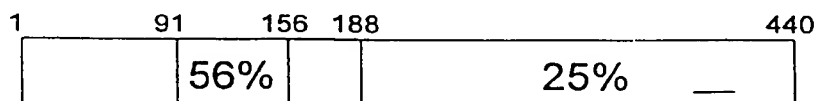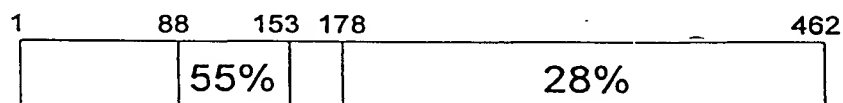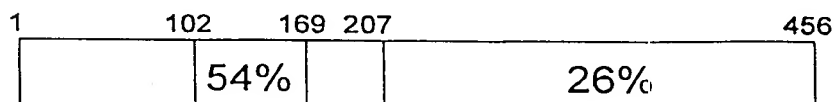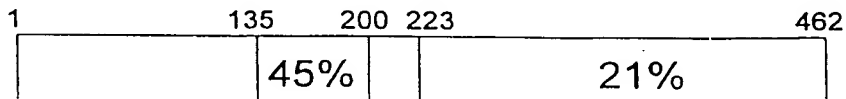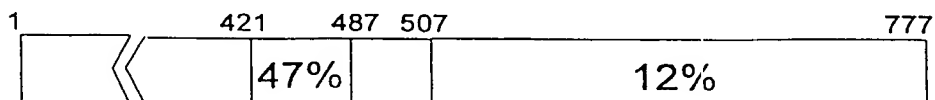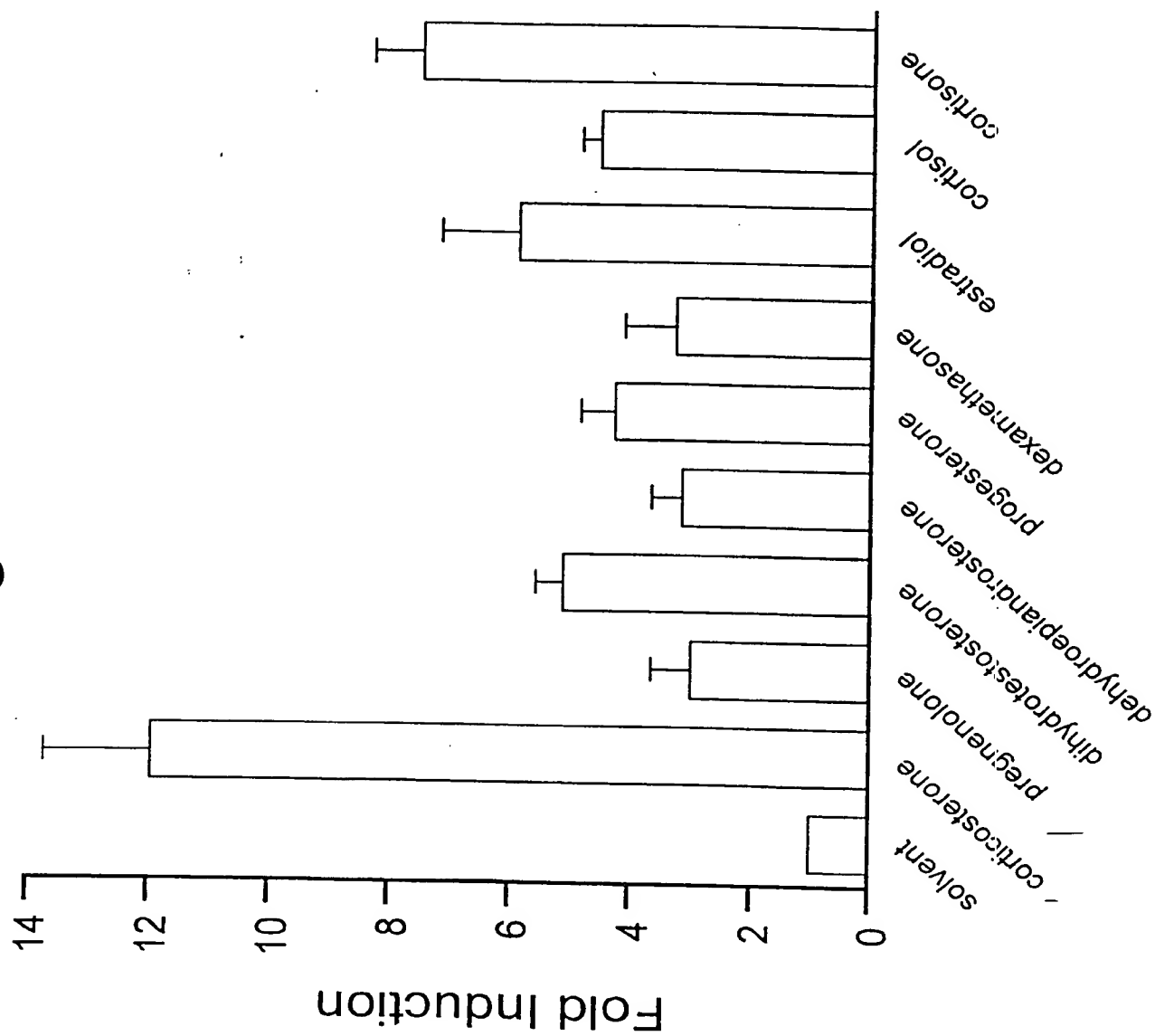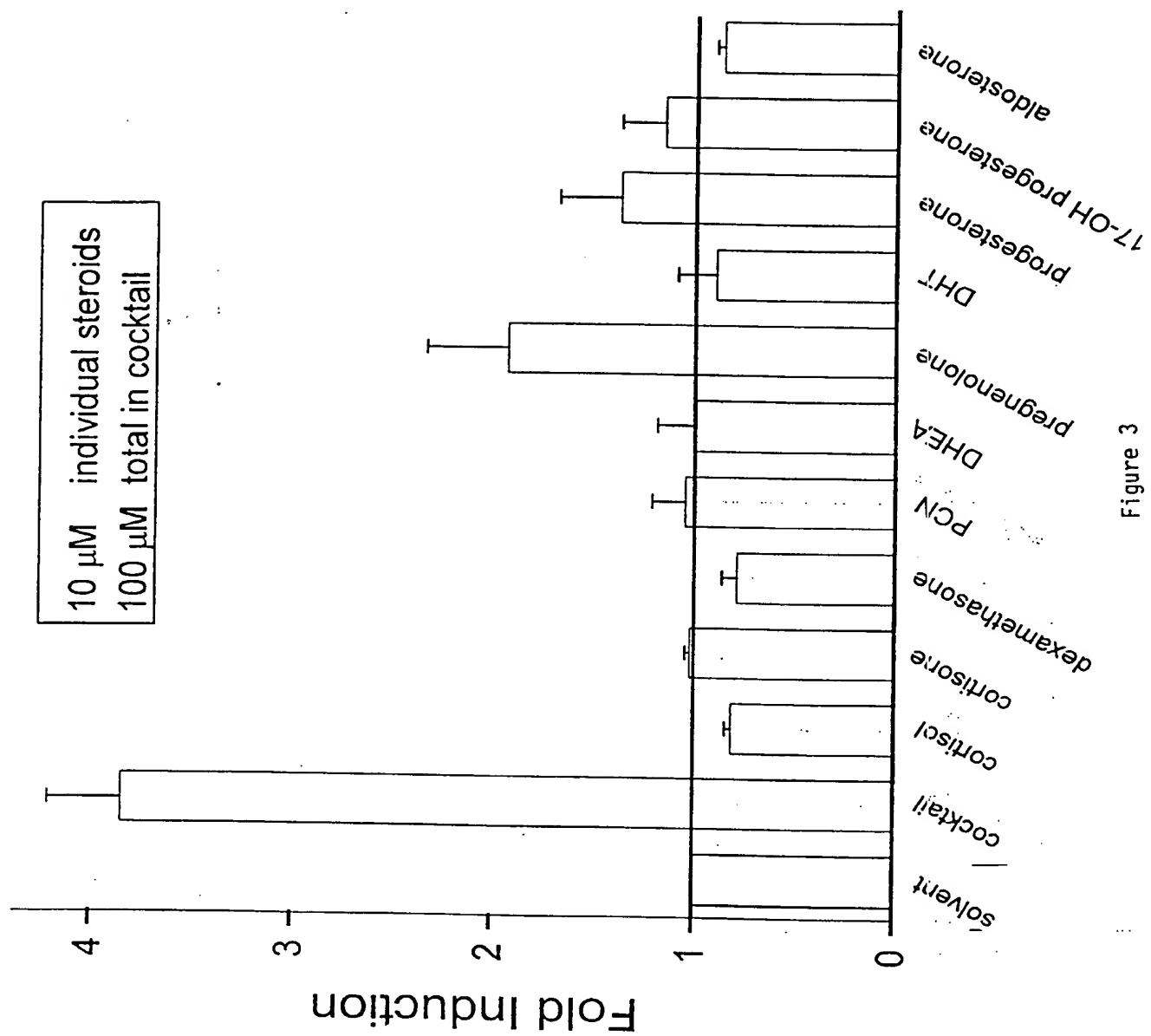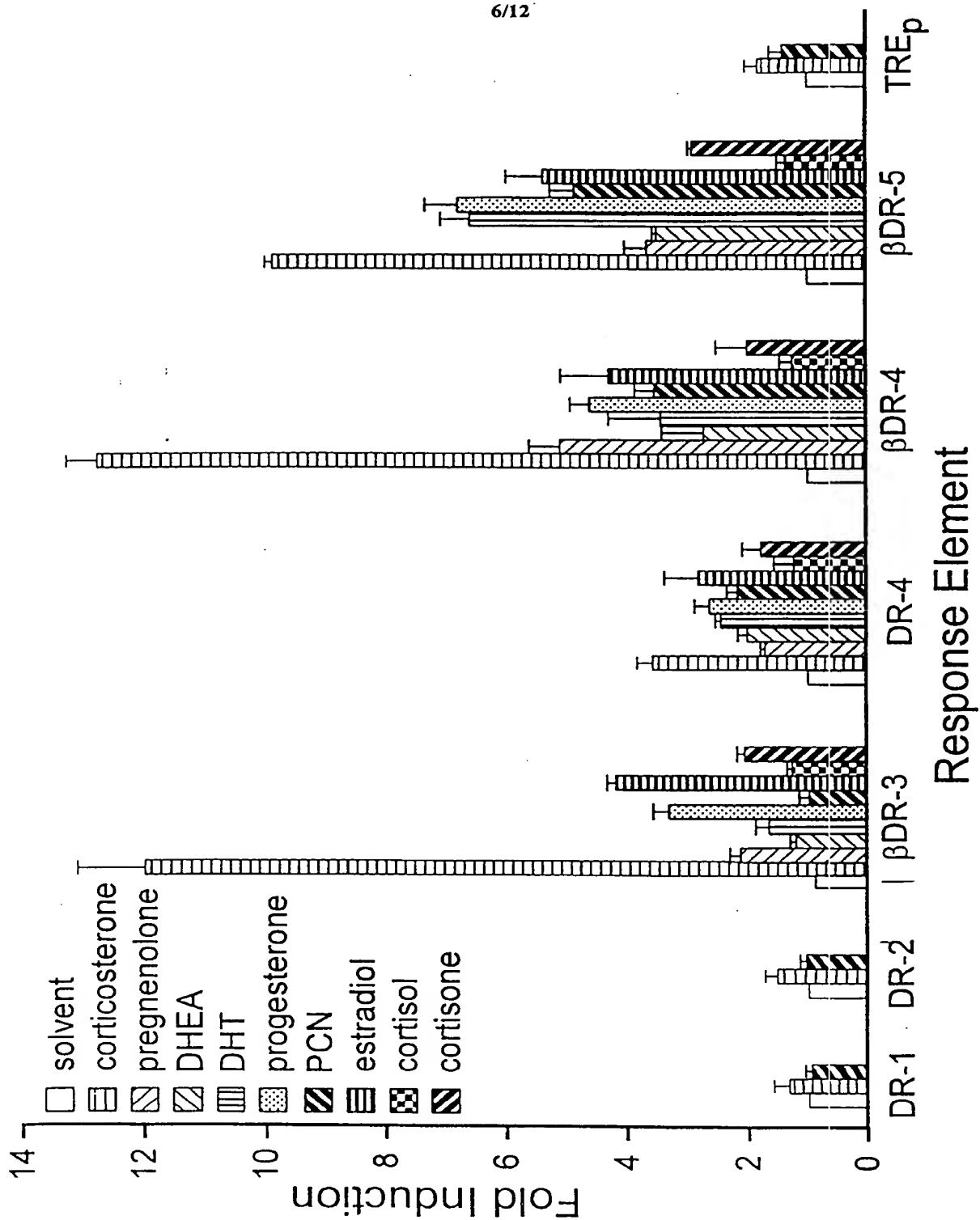
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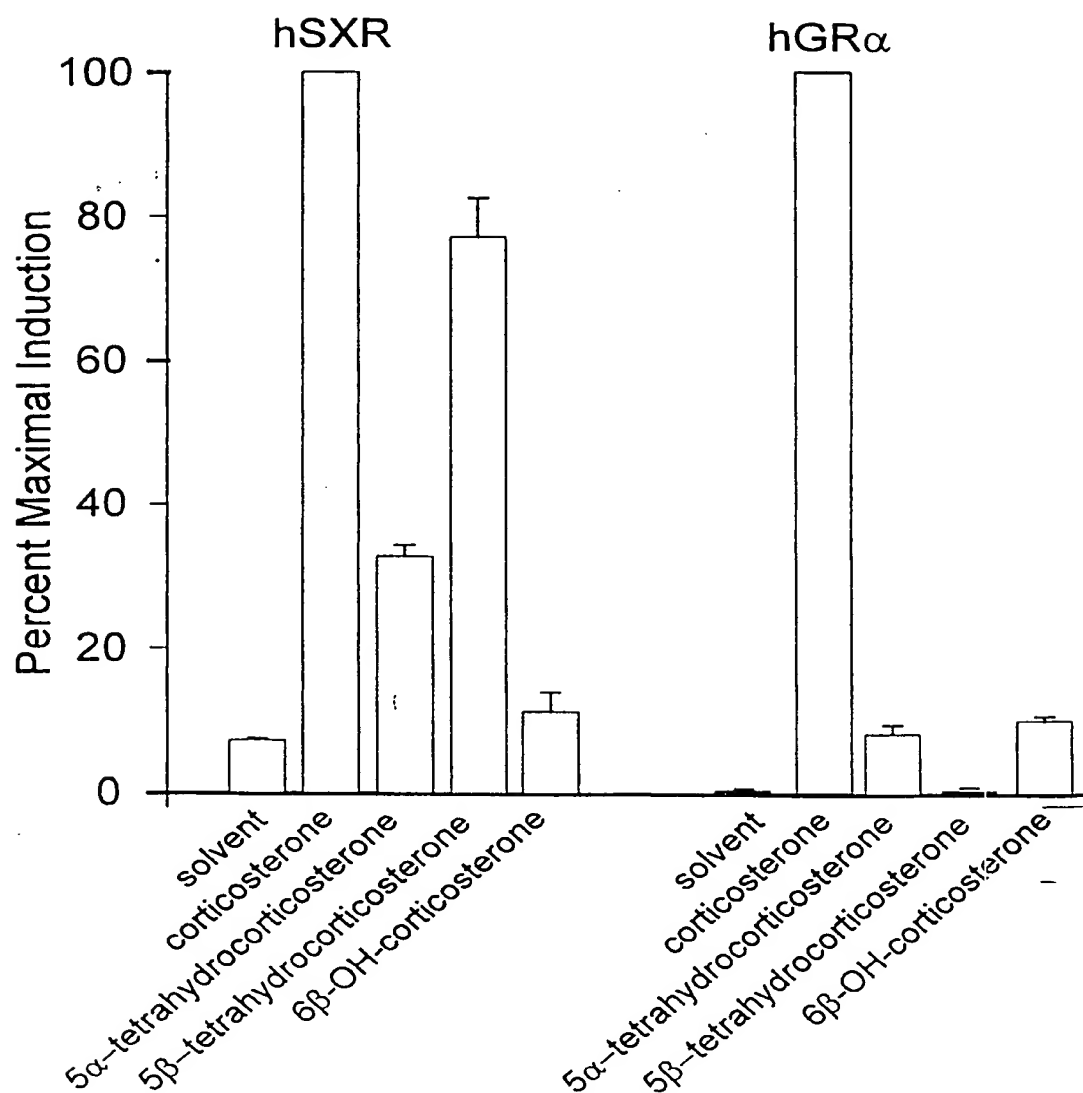
Figure 3

Figure 4

Figure 5.

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rUGT1A6   actgt **AGTTCA** taa **AGTTCA** catgg

DR-4
rbCYP2C1   caatc **AGTTCA** acag **GGTTCA** ccaat
rP450R   cac **AGGTGA** gctg **AGGCCA** gcagc **AGGTCG** aaa

DR-5
rCYP2A1   gtgca **GGTTCA** actgg **AGGTCA** acatg
rCYP2A2   gtgct **GGTTCA** actgg **AGGTCA** gtatg
rCYP2C6   agtct **AGTTCA** gtggg **GGTTCA** gtctt
hCYP2E1   gagat **GGTTCA** aggaa **GGGTCA** ttaac

Figure 6A

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```
CYP3A4    tagaata TGAACT caaagg AGGTCA gtgagtgg
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Figure 6B
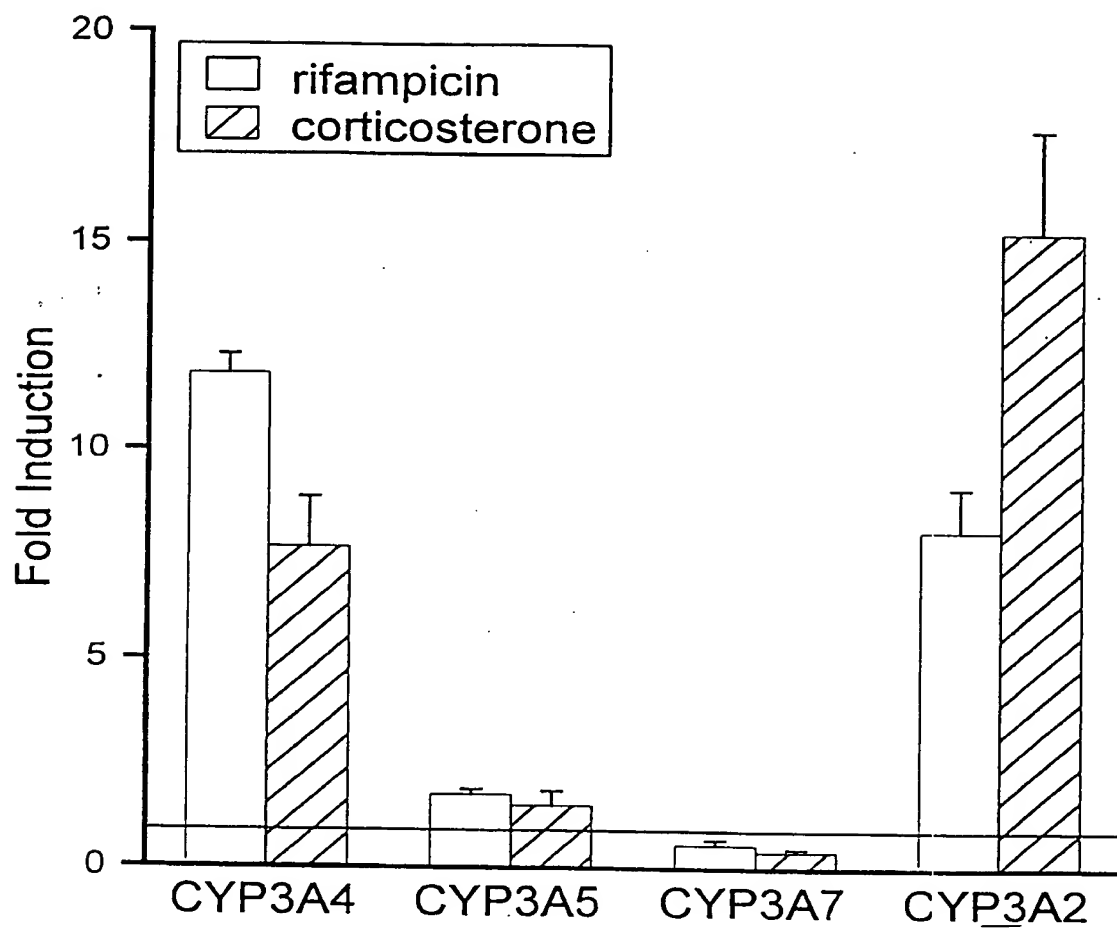
Figure 6C

Figure 7A
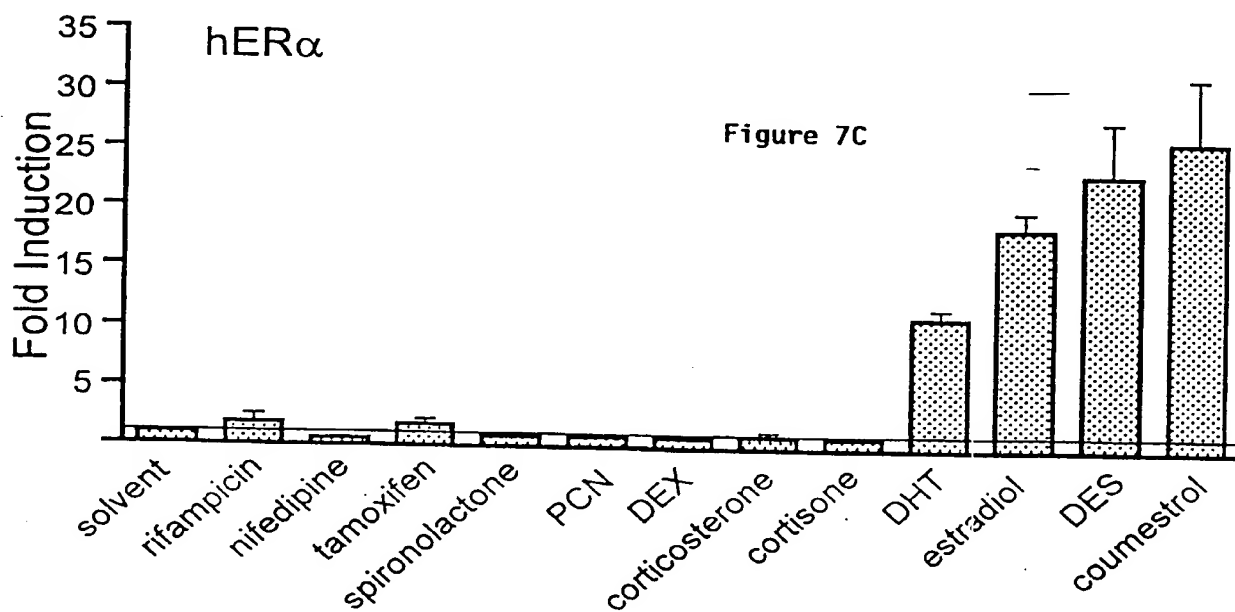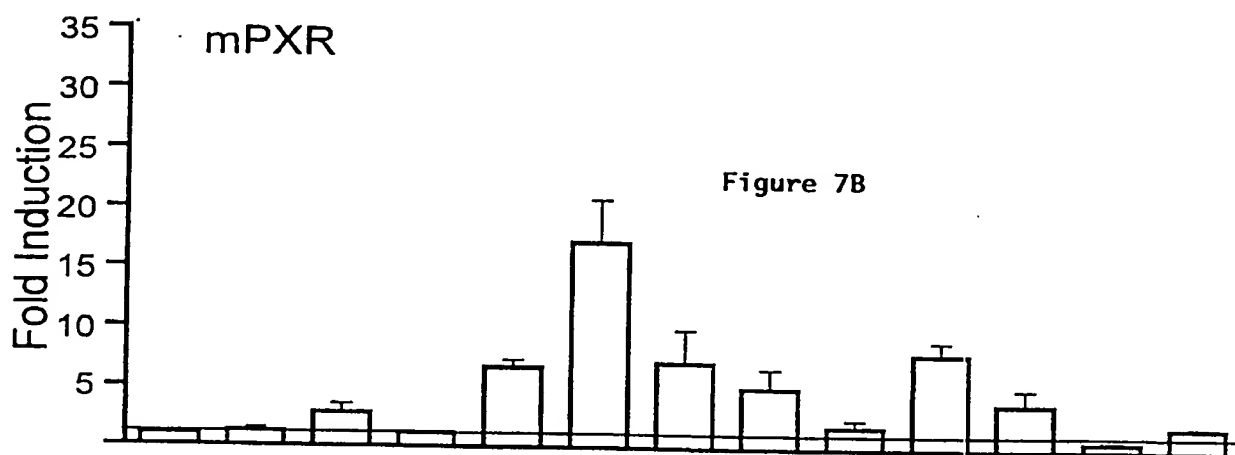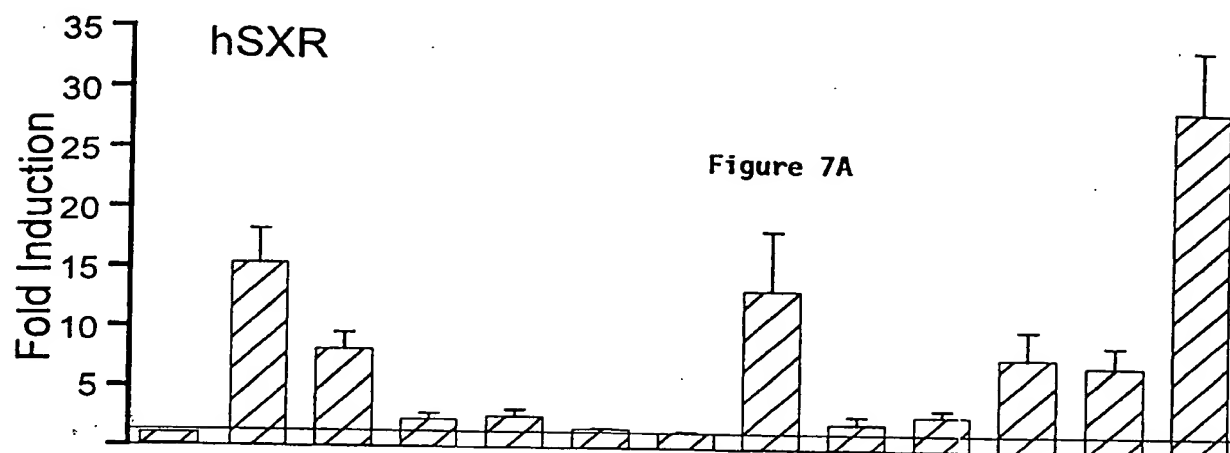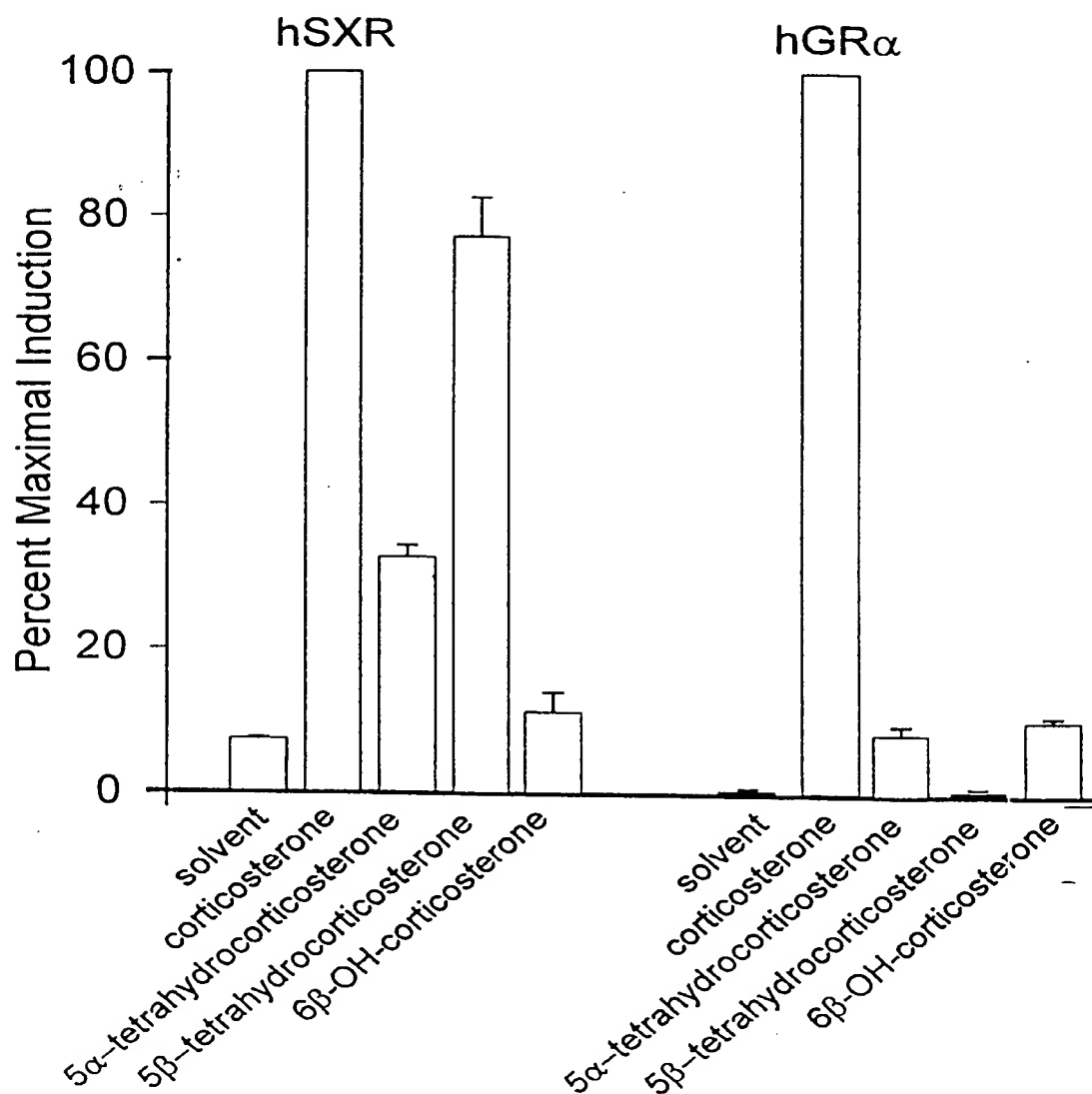
Figure 7B

Figure 7C

Figure 7D

SEQUENCE LISTING

<110> Evans, Ronald M.
      Blumberg, Bruce

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                                              Leu Glu Val Arg —
                                                1

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Pro Lys Glu Ser Trp Asn His Ala Asp Phe Val His Cys Glu Asp Thr
  5   10   15   20

gag tct gtt cct gga aag ccc agt gtc aac gca gat gag gaa gtc gga   690
Glu Ser Val Pro Gly Lys Pro Ser Val Asn Ala Asp Glu Glu Val Gly
              25   30   35

ggt ccc caa atc tgc cgt gta tgt ggg gac aag gcc act ggc tat cac   738
Gly Pro Gln Ile Cys Arg Val Cys Gly Asp Lys Ala Thr Gly Tyr His
              40   45   50

ttc aat gtc atg aca tgt gaa gga tgc aag ggc ttt ttc agg agg gcc   786

2

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Phe Asn Val Met Thr Cys Glu Gly Cys Lys Gly Phe Phe Arg Arg Ala
        55                60                65
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Met Lys Arg Asn Ala Arg Leu Arg Cys Pro Phe Arg Lys Gly Ala Cys
    70                75                80
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Glu Ile Thr Arg Lys Thr Arg Arg Gln Cys Gln Ala Cys Arg Leu Arg
85                90                95                100
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Lys Cys Leu Glu Ser Gly Met Lys Lys Glu Met Ile Met Ser Asp Glu
                105                110                115
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gcc gtg gag gag agg cgg gcc ttg atc aag cgg aag aaa agt gaa cgg       978
Ala Val Glu Glu Arg Arg Ala Leu Ile Lys Arg Lys Lys Ser Glu Arg
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Thr Phe Ser His Phe Lys Asn Phe Arg Leu Pro Gly Val Leu Ser Ser
165                170                175                180
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Gly Cys Glu Leu Pro Glu Pro Leu Gln Ala Pro Ser Arg Glu Glu Ala
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                200                205                210
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Leu Gln Ala Ala Gly Gly Gly Trp Gln Cys Leu Glu Leu Gln Xaa Pro
        215                220                225
```

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Ser Arg Gln Trp Arg Lys Glu Ile Phe Ser Leu Leu Pro His Met Ala
        230                235                240
```

```
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Asp Met Ser Thr Tyr Met Phe Lys Gly Ile Ile Ser Phe Ala Lys Val
245                250                255                260
```

```
atc tcc tac ttc agg gac ttg ccc atc gag gac cag atc tcc ctg ctg      1410
Ile Ser Tyr Phe Arg Asp Leu Pro Ile Glu Asp Gln Ile Ser Leu Leu
                265                270                275
```

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Lys Gly Ala Ala Phe Glu Leu Cys Gln Leu Arg Phe Asn Thr Val Phe
            280               285               290


aac gcg gag act gga acc tgg gag tgt ggc cgg ctg tcc tac tgc ttg    1506
Asn Ala Glu Thr Gly Thr Trp Glu Cys Gly Arg Leu Ser Tyr Cys Leu
            295               300               305


gaa gac act gca ggt ggc ttc cag caa ctt cta ctg gag ccc atg ctg    1554
Glu Asp Thr Ala Gly Gly Phe Gln Gln Leu Leu Leu Glu Pro Met Leu
            310               315               320


aaa ttc cac tac atg ctg aag aag ctg cag ctg cat gag gag gag tat    1602
Lys Phe His Tyr Met Leu Lys Lys Leu Gln Leu His Glu Glu Glu Tyr
325                 330               335               340


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Val Leu Met Gln Ala Ile Ser Leu Phe Ser Pro Asp Arg Pro Gly Val
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            360               365               370


ctg aag tcc tac att gaa tgc aat cgg ccc cag cct gct cat agg ttc    1746
Leu Lys Ser Tyr Ile Glu Cys Asn Arg Pro Gln Pro Ala His Arg Phe
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            390               395               400


gct cag cac acc cag cgg ctg ctg cgc atc cag gac ata cac ccc ttt    1842
Ala Gln His Thr Gln Arg Leu Leu Arg Ile Gln Asp Ile His Pro Phe
405                 410               415               420


gct acg ccc ctc atg cag gag ttg ttc ggc atc aca ggt agc    ___    1884
Ala Thr Pro Leu Met Gln Glu Leu Phe Gly Ile Thr Gly Ser
                425               430


tgagcggctg ccttgggtga caccttcgag aggcagccag acccagagcc ctctgagccg    1944
gcactcccgg gccaagacag atggacactg ccaagagccg acaatgccct gctggcctgt    2004
ctccctaggg aattcctgct atgacagctg gctagcattc ctcaggaagg acatggggtg    2064
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4

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Glu Glu Val Gly Gly Pro Gln Ile Cys Arg Val Cys Gly Asp Lys Ala
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Thr Gly Tyr His Phe Asn Val Met Thr Cys Glu Gly Cys Lys Gly Phe
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Phe Arg Arg Ala Met Lys Arg Asn Ala Arg Leu Arg Cys Pro Phe Arg
65                  70                  75                  80
Lys Gly Ala Cys Glu Ile Thr Arg Lys Thr Arg Arg Gln Cys Gln Ala
            85                  90                  95
Cys Arg Leu Arg Lys Cys Leu Glu Ser Gly Met Lys Lys Glu Met Ile
            100                 105                 110
Met Ser Asp Glu Ala Val Glu Glu Arg Arg Ala Leu Ile Lys Arg Lys
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Lys Ser Glu Arg Thr Gly Thr Gln Pro Leu Gly Val Gln Gly Leu Thr
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Glu Glu Gln Arg Met Met Ile Arg Glu Leu Met Asp Ala Gln Met Lys
145             ·       150                 155                 160
Thr Phe Asp Thr Thr Phe Ser His Phe Lys Asn Phe Arg Leu Pro Gly
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Val Leu Ser Ser Gly Cys Glu Leu Pro Glu Pro Leu Gln Ala Pro Ser
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Arg Glu Glu Ala Ala Lys Trp Ser Gln Val Arg Lys Asp Leu Cys Ser
            195                 200                 205
Leu Lys Val Ser Leu Gln Ala Ala Gly Gly Gly Trp Gln Cys Leu Glu
    210                 215                 220
Leu Gln Xaa Pro Ser Arg Gln Trp Arg Lys Glu Ile Phe Ser Leu Leu
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Pro His Met Ala Asp Met Ser Thr Tyr Met Phe Lys Gly Ile Ile Ser
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Phe Ala Lys Val Ile Ser Tyr Phe Arg Asp Leu Pro Ile Glu Asp Gln
            260                 265                 270
Ile Ser Leu Leu Lys Gly Ala Ala Phe Glu Leu Cys Gln Leu Arg Phe
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Asn Thr Val Phe Asn Ala Glu Thr Gly Thr Trp Glu Cys Gly Arg Leu
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Ser Tyr Cys Leu Glu Asp Thr Ala Gly Gly Phe Gln Gln Leu Leu Leu
305                 310                 315                 320
Glu Pro Met Leu Lys Phe His Tyr Met Leu Lys Lys Leu Gln Leu His
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Glu Glu Glu Tyr Val Leu Met Gln Ala Ile Ser Leu Phe Ser Pro Asp
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Arg Pro Gly Val Leu Gln His Arg Val Val Asp Gln Leu Gln Glu Gln
            355                 360                 365
Phe Ala Ile Thr Leu Lys Ser Tyr Ile Glu Cys Asn Arg Pro Gln Pro
    370                 375                 380
Ala His Arg Phe Leu Phe Leu Lys Ile Met Ala Met Leu Thr Glu Leu
385                 390                 395                 400
Arg Ser Ile Asn Ala Gln His Thr Gln Arg Leu Leu Arg Ile Gln Asp
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Ile His Pro Phe Ala Thr Pro Leu Met Gln Glu Leu Phe Gly Ile Thr
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A. CLASSIFICATION OF SUBJECT MATTER

IPC(6)   :C12N 5/12, 5/10, 15/52, 15/85, 5/22
US CL   :435/69.1, 7.1, 320.1, 252.3; 536/23.1, 24.1

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

U.S. :   435/69.1, 7.1, 320.1, 252.3; 536/23.1, 24.1

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

APS, MEDLINE, CAPLUS, WEST (DERWENT)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	US 5,639,616 A (LIAO et al.) 17 June 1997, col 1-5 and claims	1-3, 6-7, 15-20 and 22-51
Y, P	US 5,726,041 A (CHRESPI et al) 10 March, 1998, claims.	1-3, 6, 7, 15-20 and 22-51

☐ Further documents are listed in the continuation of Box C.   ☐ See patent family annex.

*	Special categories of cited documents:	"T"	later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
"A"	document defining the general state of the art which is not considered to be of particular relevance		
"B"	earlier document published on or after the international filing date	"X"	document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
"L"	document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)		
		"Y"	document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
"O"	document referring to an oral disclosure, use, exhibition or other means		
"P"	document published prior to the international filing date but later than the priority date claimed	"&"	document member of the same patent family

Date of the actual completion of the international search	Date of mailing of the international search report
01 JUNE 1999	15 JUN 1999
Name and mailing address of the ISA/US Commissioner of Patents and Trademarks Box PCT Washington, D.C. 20231	Authorized officer MARY K ZEMAN
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